

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 811.38 Seconds
(without alignments)
618.773 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380
Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTCGTGACTTT 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_nam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	38.7	50	9	AU106272
2	12	38.7	50	9	AU106275
3	12	38.7	50	9	AU106276
4	12	38.7	50	9	AU106277
5	12	38.7	50	9	AU106279
6	12	38.7	50	9	AU106287

C 7	11	35.5	25	9	AI620546
C 8	11	35.5	26	17	AZ362697
C 9	11	35.5	31	9	AI744856
C 10	11	35.5	39	9	AA757804
C 11	11	35.5	40	9	AI630923
C 12	11	35.5	49	9	AI253403
C 13	11	35.5	50	9	AU105311
C 14	10	32.3	19	17	AZ612624
C 15	10	32.3	20	17	AZ816496
C 16	10	32.3	22	9	AI664440
C 17	10	32.3	27	17	AZ783540
C 18	10	32.3	28	9	AI244530
C 19	10	32.3	29	9	AU014027
C 20	10	32.3	30	10	BE297610
C 21	10	32.3	30	17	AZ598617
C 22	10	32.3	32	9	AU014022
C 23	10	32.3	33	9	AU256484
C 24	10	32.3	33	14	T73421
C 25	10	32.3	35	14	T73795
C 26	10	32.3	37	9	AI698327
C 27	10	32.3	37	9	AA588127
C 28	10	32.3	37	17	AZ472879
C 29	10	32.3	38	17	AZ779310
C 30	10	32.3	39	14	T70882
C 31	10	32.3	39	17	AZ824330
C 32	10	32.3	39	17	BH811645
C 33	10	32.3	40	9	AI188838
C 34	10	32.3	40	9	AI684941
C 35	10	32.3	40	9	AA452094
C 36	10	32.3	45	14	T69149
C 37	10	32.3	45	14	T71655
C 38	10	32.3	46	9	AI681936
C 39	10	32.3	46	17	AZ777939
C 40	10	32.3	46	17	BH853626
C 41	10	32.3	48	17	AZ464204
C 42	10	32.3	49	9	AA130544
C 43	10	32.3	49	9	AI565007
C 44	10	32.3	49	13	BM128139
C 45	10	32.3	50	9	AU102670

ALIGNMENTS

RESULT 1	AU106272	50 bp	mRNA	linear	EST 30-AUG-2001
LOCUS	AU106272	Sugano Homo sapiens cDNA library	Homo sapiens	cDNA clone	
DEFINITION	HRC00538	mRNA sequence.			
ACCESSION	AU106272				
VERSION	AU106272.1	GI:13555793			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 50)				
	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.				
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites				
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)				
MEDLINE	21270072				
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers				


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/db_xref="taxon:9606"
/clone="HRC05583"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT      1 a      23 c      17 g      9 t
ORIGIN
Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 20 CCGCGCGCTGTT 31

RESULT 5
AUI06279
DEFINITION      50 bp mRNA linear EST 30-AUG-2001
                HRC06165, mRNA sequence.
ACCESSION      AUI06279
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
                ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
                ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
JOURNAL
MEDLINE
COMMENT      EMBO Rep. 2 (5), 388-393 (2001)
                Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: ysuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                ,S. Construction and characterization of a full length-enriched and
                a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
                source
                1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="HRC05583"
                /clone_lib="Sugano Homo sapiens cDNA library"
                /note="Differential display comparison of untreated and
                dimethylfumarate treated U937 cells"
BASE COUNT      3 a      24 c      16 g      7 t
ORIGIN
Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 6
AUI06287
DEFINITION      50 bp mRNA linear EST 30-AUG-2001
                ADSU02137, mRNA sequence.
ACCESSION      AUI06287
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
                ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
                ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
JOURNAL
MEDLINE
COMMENT      EMBO Rep. 2 (5), 388-393 (2001)
                Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: ysuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                ,S. Construction and characterization of a full length-enriched and
                a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
                source
                1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="HRC06165"
                /clone_lib="Sugano Homo sapiens cDNA library"
                /note="Differential display comparison of untreated and
                dimethylfumarate treated U937 cells"
BASE COUNT      3 a      24 c      16 g      7 t
ORIGIN
Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 7
AUI06287
DEFINITION      25 bp mRNA linear EST 15-DEC-1999
                tu95b04.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258767 3'
                similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION      AUI06287
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
TITLE      Unpublished (1997)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html
                Trace considered overall poor quality
                Insert Length: 1315 Std Error: 0.00
                Seq primer: -400P from Gibco
                High quality sequence stop: 1
                POLYA=No.

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```

SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
                ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
                ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
JOURNAL
MEDLINE
COMMENT      EMBO Rep. 2 (5), 388-393 (2001)
                Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: ysuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                ,S. Construction and characterization of a full length-enriched and
                a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
                source
                1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="ADSU02337"
                /clone_lib="Sugano Homo sapiens cDNA library"
                /note="Differential display comparison of untreated and
                dimethylfumarate treated U937 cells"
BASE COUNT      3 a      23 c      15 g      9 t
ORIGIN
Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 7
AUI06287
DEFINITION      25 bp mRNA linear EST 15-DEC-1999
                tu95b04.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258767 3'
                similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION      AUI06287
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
TITLE      Unpublished (1997)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html
                Trace considered overall poor quality
                Insert Length: 1315 Std Error: 0.00
                Seq primer: -400P from Gibco
                High quality sequence stop: 1
                POLYA=No.

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FEATURES
source

Location/Qualifiers

1. .25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2258767"
/clone_lib="NCI CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT 16 a 7 c 2 g 0 t

ORIGIN

Query Match 35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTTTCT 21

Db 22 GCTGTTTCT 12

RESULT 8

AZ362697/c

LOCUS

DEFINITION AZ362697 26 bp DNA linear GSS 02-OCT-2000
1M0107G23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0107G23 R, DNA sequence.

ACCESSION

VERSION AZ362697.1 GI:10476397

KEYWORDS

SOURCE GSS.

ORGANISM

Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 26)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0107 row: G column: 23

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0107G23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 1 a 3 c 19 g 3 t

ORIGIN

Query Match 35.5%; Score 11; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCC GCGCGCT 13

Db 11 CCCC GCGCGCT 1

RESULT 9

AI744856/c

LOCUS

DEFINITION AI744856 31 bp mRNA linear EST 21-JUN-1999
tr16all.x1 NCI CGAP Ov23 Homo sapiens CDNA clone IMAGE:2218460 3,
similar to TR:Q33564 Q33564 EATRO 184 KINETOPLAST ; contains element
TARI repetitive element ; mRNA sequence.

ACCESSION

VERSION AI744856.1 GI:5113144

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 31)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index.

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1. 31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2218460"
/clone_lib="NCI CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

19 a

3 c

7 g

2 t

BASE COUNT

ORIGIN

Query Match 35.5%; Score 11; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGTTTTCCTC 22
 Db 16 CCGTTTTCCTC 6

RESULT 10
 AA757804/c

LOCUS
 DEFINITION 39 bp mRNA linear EST 23-JAN-1998
 2944a08.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
 IMAGE:396182 3' similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN
 (HUMAN); mRNA sequence.

ACCESSION
 VERSION AA757804.1 GI:2805667
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 39)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 , J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.

AUTHORS WashU-NCI human EST Project
 Unpublished (1997)

TITLE
 JOURNAL
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1..39
 /organism="Homo sapiens"
 /db_xref="GDB:1302084"
 /db_xref="taxon:9606"
 /clone="IMAGE:396182"
 /clone_lib="Soares_pineal_gland_N3HPG"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5' TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
 , double-stranded cDNA was size selected, ligated to Eco
 RI adapters (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

BASE COUNT 15 a 3 c 10 g 11 t

ORIGIN
 Query Match 35.5%; Score 11; DB 9; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGTTTTCCTC 22
 Db 33 CCGTTTTCCTC 23

RESULT 11
 AI630923

LOCUS

DEFINITION tz31h05.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2290233 3'
 similar to SW:SP49_HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49
 ;contains TAR1.t3 MSRI repetitive element i; mRNA sequence.

ACCESSION
 VERSION AI630923.1 GI:4682253
 KEYWORDS
 SOURCE EST.
 ORGANISM human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 40)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)

AUTHORS
 TITLE Tumor Gene Index
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1907 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1..40
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2290233"
 /clone_lib="NCI_CGAP_Ut2"
 /tissue_type="moderately-differentiated endometrial
 adenocarcinoma, 3 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.85 kb. Life Technologies catalog #:
 11539-012"

BASE COUNT 2 a 26 c 8 g 4 t

ORIGIN
 Query Match 35.5%; Score 11; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGCGCGCGCT 13
 Db 4 CCGCGCGCGCT 14

RESULT 12
 AI253403

LOCUS

DEFINITION AI253403 49 bp mRNA linear EST 06-NOV-1998
 aq14c09.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone
 IMAGE:2030896 similar to FR:Q33559 Q33559 NH2 TERMINUS UNCERTAIN ;
 mRNA sequence.

ACCESSION
 VERSION AI253403.1 GI:3850358
 KEYWORDS
 SOURCE EST.
 ORGANISM human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 49)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 , J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LILNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Features Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2030896"
/clone_lib="Stanley Frontal NS pool 2"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
before use) was reverse transcribed using a modified
oligo-dT primer containing RsaI and HindIII sites.
Double-stranded cDNA was digested with RsaI, resulting in
blunt-ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
(5'-TCGAGCGCGCGCGCGGT-3' or 5'-
AGGCGTGTGGCGGCGGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
cDNA subtraction kit. Pool of two mentally normal male
individuals ages 41 and 53 (S-124, S-141) subtracted by
pool of two schizophrenic individuals, male age 44 and
female age 56 (S-116, S-118). Tissues were obtained from
the Stanley Neuropathology Consortium (www.stanleylab.org
). Library constructed and subtracted by Dr. Nancy
Johnston [(410) 614-3918, nj@weclink.vech.jhu.edu]."
BASE COUNT 5 a 11 c 6 g 27 t
ORIGIN

Query Match 35.5%; Score 11; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTTTTC TC 22
| | | | | | | |
Db 28 CTGTTTTC TC 38

RESULT 13
AUI05311/c
LOCUS 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AUI05311 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AKA01517, mRNA sequence.
ACCESSION AUI05311
VERSION AUI05311.1 GI:13554832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072

TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Features Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADKA01517"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 7 a 19 c 13 g 11 t
ORIGIN

Query Match 35.5%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGCGCGCTGT 15
| | | | | | | |
Db 17 CCGCGCGCTGT 7

RESULT 14
AZ612624
LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0439C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0439C04 R, DNA sequence.
ACCESSION AZ612624
VERSION AZ612624.1 GI:11734730
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Features Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0439C04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 5 c 7 g 7 t
ORIGIN

Query Match 32.3%; Score 10; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCTGTTT 17

DB 4 CGCGCTGTTT 13

RESULT 15
AZ816496

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ816496 20 bp DNA linear GSS 20-FEB-2001
2M0085G16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0085G16 F, DNA sequence.

AZ816496

AZ816496.1

GI:12986404

GSS.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Royagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0085 row: G column: 16

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0085G16"

/clone.lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

FEATURES
source

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 3 c 3 g 14 t
ORIGIN

Query Match 32.3%; Score 10; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTTTTTCT 21

DB 10 CTGTTTTTCT 19

Search completed: June 24, 2003, 16:52:48
Job time : 814.38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 1721.65 Seconds
(without alignments)
125.426 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31

Sequence: 1 CTCGCCGCGCGCTGTTTCTCGTCACTTT 31

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7821610 seqs, 3482903955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8654690

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
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13: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	9	US-10-359-935-22
C 2	21	67.7	28	9	US-10-359-935-29
C 3	19	61.3	19	1	PCT-US03-04088-11
C 4	19	61.3	19	1	PCT-US03-04088-275
C 5	14	45.2	25	7	US-09-954-445A-120839
C 6	14	45.2	25	7	US-09-954-445A-120843
C 7	14	45.2	25	7	US-09-954-445A-120845
C 8	14	45.2	25	12	US-60-427-808-342410
C 9	13	41.9	25	7	US-09-954-445A-31235
C 10	13	41.9	25	7	US-09-954-445A-31237
C 11	13	41.9	25	7	US-09-954-445A-31253
C 12	13	41.9	25	9	US-10-294-038-3446
C 13	13	41.9	25	9	US-10-355-577-88370
C 14	13	41.9	25	9	US-10-355-577-724663
C 15	13	41.9	25	9	US-10-355-577-738956
C 16	13	41.9	25	9	US-10-355-577-973292
C 17	13	41.9	25	10	US-10-367-892-80
C 18	13	41.9	25	10	US-10-367-892-21888
C 19	13	41.9	25	10	US-10-294-038A-3446
C 20	13	41.9	25	12	US-60-427-808-20286

C 21	13	41.9	25	12	US-60-427-808-26051	Sequence 26051, A
C 22	13	41.9	25	12	US-60-427-808-66169	Sequence 66169, A
C 23	13	41.9	25	12	US-60-427-808-583626	Sequence 583626, A
C 24	13	41.9	25	12	US-60-427-836-4638	Sequence 4638, Ap
C 25	13	41.9	25	12	US-60-427-836-105088	Sequence 105088, A
C 26	13	41.9	40	9	US-10-294-038-686	Sequence 686, App
C 27	13	41.9	40	10	US-10-294-038A-686	Sequence 686, App
C 28	12	38.7	15	9	US-10-303-778-6395	Sequence 6395, Ap
C 29	12	38.7	15	9	US-10-310-188-44983	Sequence 44983, A
C 30	12	38.7	17	9	US-10-310-188-78585	Sequence 78585, A
C 31	12	38.7	17	9	US-10-310-188-84695	Sequence 84695, A
C 32	12	38.7	18	9	US-10-303-778-5689	Sequence 5689, Ap
C 33	12	38.7	18	9	US-10-310-188-78276	Sequence 78276, A
C 34	12	38.7	19	1	PCT-US03-04088-12	Sequence 12, Appl
C 35	12	38.7	19	1	PCT-US03-04088-276	Sequence 276, App
C 36	12	38.7	19	9	US-10-310-188-85526	Sequence 85526, A
C 37	12	38.7	19	10	US-10-367-892-79	Sequence 79, Appl
C 38	12	38.7	19	10	US-10-367-892-14893	Sequence 14893, A
C 39	12	38.7	19	10	US-10-367-892-22556	Sequence 22556, A
C 40	12	38.7	20	9	US-10-348-485-21	Sequence 21, Appl
C 41	12	38.7	20	9	US-10-348-485-22	Sequence 22, Appl
C 42	12	38.7	21	9	US-10-310-188-77351	Sequence 77351, A
C 43	12	38.7	22	9	US-10-310-188-40698	Sequence 40698, A
C 44	12	38.7	25	6	US-09-660-222-63498	Sequence 63498, A
C 45	12	38.7	25	7	US-09-954-445A-87073	Sequence 87073, A

ALIGNMENTS

RESULT 1

US-10-359-935-22/c
; Sequence 22, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-10-359-935-22

Query Match 71.0%; Score 22; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 2

US-10-359-935-29/c
Sequence 29, Application US/10359935
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
Feng, Junli
Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-359-935-29

Query Match 67.7%; Score 21; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCT 21
DB 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 3

PCT-US03-04088-11
Sequence 11, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626

SOFTWARE: Patent in version 3.2

SEQ ID NO 11

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

OTHER INFORMATION: region

PCT-US03-04088-11

Query Match

Best Local Similarity 61.3%; Score 19; DB 1; Length 19;

Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCCTCCGCGCGCTGTTTTC 20
DB 1 UCCCTCCGCGCGUGUUUUC 19

RESULT 4

PCT-US03-04088-275/c
Sequence 275, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-275

Query Match 61.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TCCCGCGCGCTGTTTTC 20
DB 19 TCCCGCGCGCTGTTTTC 1

RESULT 5
US-09-954-445A-120839
; Sequence 120839, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120839

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCGCTGTTTTCCTC 22
DB 1 GCGCTGTTTTCCTC 14

RESULT 6
US-09-954-445A-120843
; Sequence 120843, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120843
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120843

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCGCTGTTTTCCTC 22
DB 9 GCGCTGTTTTCCTC 22

RESULT 7
US-09-954-445A-120845
; Sequence 120845, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120845

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCGCTGTTTTCCTC 22
DB 6 GCGCTGTTTTCCTC 19

RESULT 8
US-60-427-836-342410/C
; Sequence 342410, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 342410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-342410

Query Match 45.2%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CTGTTTTTCTCGCT 25
DB 15 CTGTTTTTCTCGCT 2

RESULT 9
US-09-954-445A-31235
; Sequence 31235, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1

; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31253
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31253

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26
|||||
DB 6 GTTTTCTCGCTG 18

RESULT 10
US-09-954-445A-31237
; Sequence 31237, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31237

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26
|||||
DB 2 GTTTTCTCGCTG 14

RESULT 11
US-09-954-445A-31253
; Sequence 31253, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31253
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31253

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26

DB 12 GTTTTCTCGCTG 24
|||||

RESULT 12
US-10-294-038-3446/c
; Sequence 3446, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 3446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1583792)...(1583815)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4331
US-10-294-038-3446

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTCTCGCTGAC 28
|||||
DB 18 TTTTCTCGCTGAC 6

RESULT 13
US-10-355-577-88370
; Sequence 88370, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-88370

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTTTCTCGCTG 25
|||||
DB 12 TTTTCTCGCTG 24

RESULT 14
US-10-355-577-724663
; Sequence 724663, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 724663
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Homo sapien
US-10-355-577-724663

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTTCCTCGCT 25
|||||
Db 4 TGTTCCTCGCT 16

RESULT 15

US-10-355-577-738956
; Sequence 738956, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 738956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-738956

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTTCCTCGCT 25
|||||
Db 13 TGTTCCTCGCT 25

Search completed: June 24, 2003, 20:14:43
Job time : 1721.65 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:01:44 ; Search time 1340.69 Seconds
(without alignments)
581.357 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31

Sequence: 1 CTCGCCGCGCGCTGTTTCTCGCTGACTTT 31

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	6	US-08-272-102-22
C 2	22	71.0	30	7	US-08-387-524-18
C 3	22	71.0	30	8	US-08-472-802A-23
C 4	22	71.0	30	8	US-08-472-802B-23
C 5	22	71.0	30	8	US-08-482-115A-22
C 6	22	71.0	30	9	US-08-520-550-18
C 7	22	71.0	30	9	US-08-521-634-40
C 8	22	71.0	30	10	US-08-660-678-22
C 9	22	71.0	30	14	US-09-057-351-22
C 10	22	71.0	30	16	US-09-259-943-44
C 11	21	67.7	28	8	US-08-472-802A-29
C 12	21	67.7	28	8	US-08-472-802B-29
C 13	21	67.7	28	8	US-08-482-115A-28
C 14	21	67.7	28	9	US-08-521-634-47
C 15	21	67.7	28	14	US-09-057-351-29
C 16	21	67.7	30	7	US-08-387-524-34
C 17	21	67.7	30	9	US-08-520-550-34
C 18	21	67.7	30	16	US-09-259-943-60
C 19	17	54.8	22	16	US-09-259-943-25
C 20	17	54.8	26	9	US-08-521-634-8
C 21	14	45.2	22	1	PCT-US99-07886-52

22 14 45.2 22 1 PCT-US99-07886-52
 23 14 45.2 22 14 US-09-058-968-52
 24 14 45.2 25 67 US-60-233-620-120839
 25 14 45.2 25 67 US-60-233-620-120843
 26 14 45.2 25 67 US-60-233-620-120845
 27 14 45.2 28 9 US-08-521-634-7
 28 14 45.2 42 18 US-09-404-520-38793
 29 13 41.9 20 23 US-09-601-267-31
 30 13 41.9 20 23 US-09-601-267-34
 31 13 41.9 25 1 PCT-US02-25940-80
 32 13 41.9 25 1 PCT-US02-25940-1888
 33 13 41.9 25 36 US-09-956-584-71299
 34 13 41.9 25 36 US-09-956-584-71303
 35 13 41.9 25 36 US-09-956-604-28714
 36 13 41.9 25 36 US-09-956-604-28716
 37 13 41.9 25 36 US-09-956-604-28717
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 39 13 41.9 25 36 US-09-956-604-28719
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 41 13 41.9 25 36 US-09-956-604-28757
 42 13 41.9 25 36 US-09-956-604-28758
 43 13 41.9 25 36 US-09-956-604-28760
 44 13 41.9 25 36 US-09-956-604-28762
 45 13 41.9 25 36 US-09-956-604A-28714

ALIGNMENTS

RESULT 1
 US-08-272-102-22/c
 ; Sequence 22, Application US/08272102
 ; GENERAL INFORMATION:
 ; APPLICANT: VILLEPONTEAU, Bryant
 ; APPLICANT: FENG, Junli
 ; APPLICANT: FUNK, Walter
 ; APPLICANT: ANDREWS, William H.
 ; TITLE OF INVENTION: HUMAN TELOMERASE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/272,102
 ; FILING DATE: 07-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15389-000800
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-272-102-22

Query Match 71.0%; Score 22; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.068;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCCTCCGCGCGCTGTTTTCTC 22
 Db 22 CTCCTCCGCGCGCTGTTTTCTC 1
 RESULT 2
 US-08-387-524-18/c
 ; Sequence 18, Application US/08387524
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrews, William H.
 ; APPLICANT: Avilion, Ariel A.
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Greider, Carol
 ; APPLICANT: Marhuenda, Maria A. B.
 ; APPLICANT: Villeponteau, Bryant
 ; TITLE OF INVENTION: RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/387,524
 ; FILING DATE: 13-FEB-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL94-05A3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-387-524-18

Query Match 71.0%; Score 22; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCCTCCGCGCGCTGTTTTCTC 22
 Db 22 CTCCTCCGCGCGCTGTTTTCTC 1

RESULT 3
 US-08-472-802A-23/c
 ; Sequence 23, Application US/08472802A
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli

APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802A-23

Query Match 71.0%; Score 22; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 4

US-08-472-802B-23/c
Sequence 23, Application US/08472802B
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,802B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802B-23

Query Match 71.0%; Score 22; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 5

US-08-482-115A-22/c
Sequence 22, Application US/08482115A
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-482-115A-22

Query Match 71.0%; Score 22; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.068;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22

DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 6

US-08-520-550-18/c

Sequence 18, Application US/08520550

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avilion, Ariel A.

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria A. B.

APPLICANT: Villeponteau, Bryant

TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,550

FILING DATE: 29-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524

FILING DATE: 13-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHU94-05A3B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-520-550-18

Query Match

Best Local Similarity 71.0%; Score 22; DB 9; Length 30;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22

DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 7

US-08-521-634-40/c

Sequence 40, Application US/08521634

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/521,634

FILING DATE: 31-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,115

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 7-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dunn, Tracy J.

REGISTRATION NUMBER: 34,587

REFERENCE/DOCKET NUMBER: 15389-000850

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)

US-08-521-634-40

Query Match

Best Local Similarity 71.0%; Score 22; DB 9; Length 30;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22

DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 8

US-08-660-678-22/c

Sequence 22, Application US/08660678

```

; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/660,678
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 15389-000811
; REFERENCE/DOCKET NUMBER: 15389-000811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678-22

Query Match 71.0%; Score 22; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTTCTC 1

RESULT 9
US-09-057-351-22/c
; Sequence 22, Application US/09057351
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-22

Query Match 71.0%; Score 22; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTTCTC 1

RESULT 10
US-09-259-943-44/c
; Sequence 44, Application US/09259943
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A.B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; FILE REFERENCE: CSHL94-05A7
; CURRENT APPLICATION NUMBER: US/09/259,943
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/623,166
; EARLIER FILING DATE: 1996-03-28
; EARLIER APPLICATION NUMBER: 08/520,550
; EARLIER FILING DATE: 1995-08-29
; EARLIER APPLICATION NUMBER: 08/485,778
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/387,524
; EARLIER FILING DATE: 1995-02-13
; EARLIER APPLICATION NUMBER: 08/330,123
; EARLIER FILING DATE: 1994-10-27
; EARLIER APPLICATION NUMBER: 08/272,102
; EARLIER FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 30
; TYPE: DNA

```

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotides
US-09-259-943-44

Query Match 71.0%; Score 22; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 11
US-08-472-802A-29/c
; Sequence 29, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-29

Query Match 67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 13
US-08-482-115A-28/c
; Sequence 28, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic oligonucleotides
US-09-259-943-44

Query Match 71.0%; Score 22; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 11
US-08-472-802A-29/c
; Sequence 29, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-29

Query Match 67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 12
US-08-472-802B-29/c

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-28

Query Match 67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 14
US-08-521-634-47/c
Sequence 47, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-47

Query Match 67.7%; Score 21; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 15
US-09-057-351-29/c
Sequence 29, Application US/09057351
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-29
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Query Match 67.7%; Score 21; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTCCTCGCGCGCTGTTTCT 21
   |||||
Db 21 CTCCTCGCGCGCTGTTTCT 1
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Search completed: June 24, 2003, 18:22:28
Job time : 1340.69 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:29:49 ; Search time 377.636 Seconds
(without alignments)
120.460 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTCGTGACTTT 31

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	21	67.7	28	10	US-09-057-351-29
C 3	12	38.7	19	10	US-09-969-373-3585
C 4	12	38.7	20	9	US-09-932-367A-36
C 5	12	38.7	25	9	US-09-992-665-170
C 6	12	38.7	25	9	US-10-098-263B-48907
C 7	12	38.7	28	9	US-09-932-367A-89
C 8	12	38.7	28	9	US-09-932-367A-98
C 9	12	38.7	43	9	US-09-944-160-17
C 10	11	35.5	21	9	US-10-175-225-84
C 11	11	35.5	25	9	US-10-098-263B-15754
C 12	11	35.5	25	9	US-10-098-263B-18868
C 13	11	35.5	25	9	US-10-098-263B-36074
C 14	11	35.5	25	9	US-10-098-263B-47761
C 15	11	35.5	25	9	US-10-098-263B-48908
C 16	11	35.5	25	9	US-10-098-263B-54070
C 17	11	35.5	25	9	US-10-098-263B-60378
C 18	11	35.5	25	9	US-10-098-263B-63628
C 19	11	35.5	25	9	US-10-098-263B-118879

C 20	11	35.5	25	9	US-10-098-263B-118880
C 21	11	35.5	25	9	US-10-098-263B-120100
C 22	11	35.5	25	9	US-10-098-263B-121313
C 23	11	35.5	25	9	US-10-098-263B-121314
C 24	11	35.5	29	9	US-09-932-367A-84
C 25	11	35.5	31	9	US-09-870-759-145
C 26	11	35.5	35	9	US-10-001-189-12
C 27	11	35.5	40	9	US-09-769-787-385
C 28	11	35.5	40	10	US-09-245-802-84
C 29	11	35.5	40	10	US-09-245-802-129
C 30	10	32.3	18	10	US-09-870-162A-40
C 31	10	32.3	19	10	US-09-018-125-2
C 32	10	32.3	20	9	US-09-909-595-18
C 33	10	32.3	20	9	US-10-238-443-42
C 34	10	32.3	20	9	US-10-016-149-51
C 35	10	32.3	20	9	US-09-953-318-76
C 36	10	32.3	20	10	US-09-810-560-6
C 37	10	32.3	21	9	US-10-090-011-7
C 38	10	32.3	21	9	US-10-044-692-237
C 39	10	32.3	21	9	US-10-044-539-237
C 40	10	32.3	21	10	US-09-885-441-54
C 41	10	32.3	22	9	US-09-978-295A-543
C 42	10	32.3	22	9	US-09-978-697-543
C 43	10	32.3	22	9	US-09-978-192A-543
C 44	10	32.3	22	9	US-09-999-832A-543
C 45	10	32.3	22	9	US-09-978-189-543

ALIGNMENTS

RESULT 1
US-09-057-351-22/c
; Sequence 22, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Vilpeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

Query Match 67.7%; Score 21; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0077;

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Query Match      38.7%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 18 CTCCTCCGCGCGC 7

RESULT 5

US-09-992-665-170/c
 ; Sequence 170, Application US/09992665
 ; Publication No. US20030092009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaia Palm
 ; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ; FILE REFERENCE: CEMINS.002A
 ; CURRENT APPLICATION NUMBER: US/09/992,665
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: 60/249,508
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 170
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-09-992-665-170

Query Match 38.7%; Score 12; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. le+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 23 CTCCTCCGCGCGC 12

RESULT 6

US-10-098-263B-48907
 ; Sequence 48907, Application US/10098263B
 ; Publication No. US2003010410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 48907
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-48907

Query Match 38.7%; Score 12; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. le+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCT 25
 Db 13 GTTTTCTCGCT 24

RESULT 7

US-09-932-367A-89/c
 ; Sequence 89, Application US/09932367A
 ; Publication No. US20030027152A1
 ; GENERAL INFORMATION:

; APPLICANT: RHODES, Simon J.
 ; APPLICANT: BRIDWELL, Jeanne L.
 ; APPLICANT: MEIER, Bradley C.
 ; APPLICANT: PARKER, Gretchen E.
 ; APPLICANT: PRICE, Jeffrey R.
 ; APPLICANT: SHOWALTER, Aaron D.
 ; APPLICANT: SLOOP, Kyle W.
 ; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
 ; FILE REFERENCE: LHX3/P-LIM/LIM-3 FACTOR
 ; CURRENT APPLICATION NUMBER: US/09/932,367A
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/04424
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/121,110
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 89
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
 US-09-932-367A-89

Query Match 38.7%; Score 12; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. le+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 26 CTCCTCCGCGCGC 15

RESULT 8

US-09-932-367A-98/c
 ; Sequence 98, Application US/09932367A
 ; Publication No. US20030027152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODES, Simon J.
 ; APPLICANT: BRIDWELL, Jeanne L.
 ; APPLICANT: MEIER, Bradley C.
 ; APPLICANT: PARKER, Gretchen E.
 ; APPLICANT: PRICE, Jeffrey R.
 ; APPLICANT: SHOWALTER, Aaron D.
 ; APPLICANT: SLOOP, Kyle W.
 ; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
 ; FILE REFERENCE: LHX3/P-LIM/LIM-3 FACTOR
 ; CURRENT APPLICATION NUMBER: US/09/932,367A
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/04424
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/121,110
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 98
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
 US-09-932-367A-98

Query Match 38.7%; Score 12; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. le+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 26 CTCCTCCGCGCGC 15

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RESULT 9
US-09-944-160-17/c
; Sequence 17, Application US/09944160
; Patent No. US20020174452A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. US20020174452Alman
; APPLICANT: Davin, Laurence
; APPLICANT: .. Huang, Ning
; TITLE OF INVENTION: Monocot Seeds with Increased Lignan
; TITLE OF INVENTION: Content
; FILE REFERENCE: WSUR117983
; CURRENT APPLICATION NUMBER: US/09/944,160
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/230,632
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-944-160-17

Query Match      38.7%; Score 12; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTTTTTCTCG 23
DB 32 CTGTTTTTCTCG 21

RESULT 10
US-10-175-225-84/c
; Sequence 84, Application US/10175225
; Publication No. US20030082582A1
; GENERAL INFORMATION:
; APPLICANT: Richard A. Gatti
; TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
; TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
; FILE REFERENCE: UC078.001DVI
; CURRENT APPLICATION NUMBER: US/10/175,225
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 09/360,416
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-10-175-225-84

Query Match      35.5%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTTTTTCT 21
DB 19 GCTGTTTTTCT 9

RESULT 11
US-10-098-263B-15754
; Sequence 15754, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray

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; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 15754
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-15754

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTTTTCTCG 23
DB 13 TGTGTTTTCTCG 23

RESULT 12
US-10-098-263B-18868/c
; Sequence 18868, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18868
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-18868

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTCTCGCTG 26
DB 22 TTTTCTCGCTG 12

RESULT 13
US-10-098-263B-36074
; Sequence 36074, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 36074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-36074

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGCTG 14
|||||
Db 5 CCGCGCGCTG 15

RESULT 14

US-10-098-263B-47761/c
; Sequence 47761, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 47761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-47761

Query Match 35.5%; Score 11; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CTCGCTGACTT 30
|||||
Db 18 CTCGCTGACTT 8

RESULT 15

US-10-098-263B-48908
; Sequence 48908, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-48908

Query Match 35.5%; Score 11; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTTTCTCGCT 25
|||||
Db 14 TTTTCTCGCT 24

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Job time : 378.636 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 19:12:24 ; Search time 29.719 Seconds
(without alignments)
319.896 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgn2_6/ptodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS-COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	1 US-08-330-123A-22	Sequence 22, Appl
C 2	22	71.0	30	1 US-08-482-115B-22	Sequence 22, Appl
C 3	22	71.0	30	2 US-08-660-678A-22	Sequence 22, Appl
C 4	22	71.0	30	2 US-08-485-778-18	Sequence 18, Appl
C 5	22	71.0	30	2 US-08-472-802C-23	Sequence 23, Appl
C 6	22	71.0	30	3 US-08-520-550A-18	Sequence 18, Appl
C 7	22	71.0	30	3 US-08-998-443-22	Sequence 22, Appl
C 8	22	71.0	30	4 US-09-060-523-22	Sequence 22, Appl
C 9	22	71.0	30	4 US-09-580-517-22	Sequence 22, Appl
C 10	21	67.7	28	1 US-08-482-115B-28	Sequence 28, Appl
C 11	21	67.7	28	2 US-08-472-802C-29	Sequence 29, Appl
C 12	21	67.7	30	2 US-08-485-778-34	Sequence 34, Appl
C 13	21	67.7	30	3 US-08-520-550A-34	Sequence 34, Appl
C 14	12	38.7	20	1 US-08-089-996-21	Sequence 21, Appl
C 15	12	38.7	20	1 US-08-089-996-22	Sequence 22, Appl
C 16	12	38.7	20	2 US-08-478-178A-21	Sequence 21, Appl
C 17	12	38.7	20	2 US-08-478-178A-22	Sequence 22, Appl
C 18	12	38.7	20	2 US-08-488-177-21	Sequence 21, Appl
C 19	12	38.7	20	2 US-08-488-177-22	Sequence 22, Appl
C 20	12	38.7	20	2 US-08-481-072A-21	Sequence 21, Appl
C 21	12	38.7	20	2 US-08-481-072A-22	Sequence 22, Appl
C 22	12	38.7	20	2 US-08-664-336-21	Sequence 21, Appl
C 23	12	38.7	20	2 US-08-664-336-22	Sequence 22, Appl
C 24	12	38.7	20	2 US-08-481-066A-21	Sequence 21, Appl
C 25	12	38.7	20	2 US-08-481-066A-22	Sequence 22, Appl
C 26	12	38.7	20	3 US-08-578-615A-21	Sequence 21, Appl
C 27	12	38.7	20	3 US-08-578-615A-22	Sequence 22, Appl

C 28	12	38.7	20	4 US-08-829-637A-21	Sequence 21, Appl
C 29	12	38.7	20	4 US-08-829-637A-22	Sequence 22, Appl
C 30	12	38.7	20	4 US-09-254-322-21	Sequence 21, Appl
C 31	12	38.7	20	4 US-09-254-322-22	Sequence 22, Appl
C 32	12	38.7	20	5 PCT-US93-02213-21	Sequence 21, Appl
C 33	12	38.7	20	5 PCT-US93-02213-22	Sequence 22, Appl
C 34	12	38.7	20	5 PCT-US94-07770-21	Sequence 21, Appl
C 35	12	38.7	20	5 PCT-US94-07770-22	Sequence 22, Appl
C 36	12	38.7	22	4 US-08-564-989-8	Sequence 8, Appl
C 37	11	35.5	20	1 US-08-534-975-12	Sequence 12, Appl
C 38	11	35.5	20	2 US-08-954-470-12	Sequence 12, Appl
C 39	11	35.5	20	3 US-09-129-855A-12	Sequence 12, Appl
C 40	11	35.5	20	4 US-09-444-053-39	Sequence 39, Appl
C 41	11	35.5	20	4 US-09-247-154-12	Sequence 12, Appl
C 42	11	35.5	20	4 US-09-306-405-68	Sequence 68, Appl
C 43	11	35.5	20	4 US-09-480-718-12	Sequence 12, Appl
C 44	11	35.5	21	1 US-08-753-147-65	Sequence 65, Appl
C 45	11	35.5	21	4 US-09-360-416-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-08-330-123A-22/c
; Sequence 22, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/330,123A
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-22

Query Match 71.0%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTC 22
Db 22 CTCCTCCGCGCGCTGTTTTC 1

RESULT 2

US-08-482-115B-22/c
; Sequence 22, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-22

Query Match 71.0%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTC 22
Db 22 CTCCTCCGCGCGCTGTTTTC 1

RESULT 3

US-08-660-678A-22/c
; Sequence 22, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-22

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTC 22
Db 22 CTCCTCCGCGCGCTGTTTTC 1

RESULT 4

US-08-485-778-18/c
; Sequence 18, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-18

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 5
US-08-472-802C-23/c
Sequence 23, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Vilponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-23

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 6
US-08-520-550A-18/c
Sequence 18, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Vilponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-18

Query Match 71.0%; Score 22; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 7
US-08-998-443-22/c
; Sequence 22, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Query Match 71.0%; Score 22; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 8
US-09-060-523-22/c
; Sequence 22, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-060-523-22

Query Match 71.0%; Score 22; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 9
US-09-580-517-22/c
; Sequence 22, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-580-517-22

Query Match 71.0%; Score 22; DB 4; Length 30;
Best Local Similarity: 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 10
US-08-482-115B-28/c
Sequence 28, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-28
Query Match 67.7%; Score 21; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCCGCGCGCTGTTTCT 21
DB 21 CTCCTCCGCGCGCTGTTTCT 1
RESULT 11
US-08-472-802C-29/c
Sequence 29, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-29

Query Match 67.7%; Score 21; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTGGCGCTGTTTCT 21
DB 21 CTCCTGGCGCTGTTTCT 1

RESULT 12
US-08-485-778-34
; Sequence 34, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 67.7%; Score 21; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QX 9 GCGCTGTTTCTCGCTGACT 29

DB 10 GCGCTGTTTCTCGCTGACT 30

RESULT 13
US-08-520-550A-34
; Sequence 34, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 67.7%; Score 21; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCTGTTTCTCGCTGACT 29
DB 10 GCGCTGTTTCTCGCTGACT 30

RESULT 14
US-08-089-996-21/c
; Sequence 21, Application US/08089996
; Patent No. 5703054
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett

;; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
;; TITLE OF INVENTION: Kinase C
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & No. 5703054ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/089,996
;; FILING DATE: 19930709
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 852,852
;; FILING DATE: March 16, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rebecca Ralph Gaumont
;; REGISTRATION NUMBER: 35,152
;; REFERENCE/DOCKET NUMBER: ISIS-1154
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: yes
US-08-089-996-21

Query Match 38.7%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
Db 18 CTCCTCCGCGCGC 7

RESULT 15
US-08-089-996-22/c
;; Sequence 22, Application US/08089996
;; Patent No. 5703054
;; GENERAL INFORMATION:
;; APPLICANT: Nicholas Dean, C. Frank Bennett
;; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
;; TITLE OF INVENTION: Kinase C
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & No. 5703054ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/089,996
;; FILING DATE: 19930709

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 852,852
;; FILING DATE: March 16, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rebecca Ralph Gaumont
;; REGISTRATION NUMBER: 35,152
;; REFERENCE/DOCKET NUMBER: ISIS-1154
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: yes
US-08-089-996-22

Query Match 38.7%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
Db 13 CTCCTCCGCGCGC 2

Search completed: June 24, 2003, 16:54:55
Job time : 30.719 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:14:29 ; Search time 117.339 Seconds
(without alignments)
594.960 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31

Sequence: 1 CTCGCCGCGCTGTTTCTTCGCTGACTTT 31

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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15: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
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18: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	17	AA10298
C 2	22	71.0	30	17	AA11043
C 3	21	67.7	30	17	AA11059
C 4	14	45.2	22	20	AAZ33130
C 5	13	41.9	20	20	AAZ07291
C 6	13	41.9	20	20	AAZ07294
C 7	13	41.9	22	21	AAZ29625
C 8	13	41.9	28	24	ABL60273
C 9	13	41.9	29	20	AAZ07292

C 1	22	71.0	30	17	AA10298
C 2	22	71.0	30	17	AA11043
C 3	21	67.7	30	17	AA11059
C 4	14	45.2	22	20	AAZ33130
C 5	13	41.9	20	20	AAZ07291
C 6	13	41.9	20	20	AAZ07294
C 7	13	41.9	22	21	AAZ29625
C 8	13	41.9	28	24	ABL60273
C 9	13	41.9	29	20	AAZ07292

C 1	22	71.0	30	17	AA10298
C 2	22	71.0	30	17	AA11043
C 3	21	67.7	30	17	AA11059
C 4	14	45.2	22	20	AAZ33130
C 5	13	41.9	20	20	AAZ07291
C 6	13	41.9	20	20	AAZ07294
C 7	13	41.9	22	21	AAZ29625
C 8	13	41.9	28	24	ABL60273
C 9	13	41.9	29	20	AAZ07292

RNA component of h
Primer for product
Treponema pallidum
Mouse telomerase R
Mouse telomerase R
Tick derived cyste
Borrelia burgdorfe
Mouse telomerase R

C 10	12	38.7	15	24	AAS98334	Galanin receptor g
C 11	12	38.7	15	24	AAS98336	Galanin receptor g
C 12	12	38.7	15	24	AAS98341	Galanin receptor g
C 13	12	38.7	20	14	AAO49677	PKC-beta type I an
C 14	12	38.7	20	14	AAO49678	PKC-beta type I an
C 15	12	38.7	20	16	AAQ97894	PNA oligomer targe
C 16	12	38.7	20	16	AAQ97895	PNA oligomer targe
C 17	12	38.7	20	16	AAQ84181	PKC-beta type I an
C 18	12	38.7	20	16	AAQ84182	PKC-beta type I an
C 19	12	38.7	20	19	AAV35521	Oligo ON21 targete
C 20	12	38.7	20	19	AAV35522	Oligo ON22 targete
C 21	12	38.7	20	20	AAZ27286	Human protein kina
C 22	12	38.7	20	20	AAZ27287	Human protein kina
C 23	12	38.7	20	20	AAZ78544	Human PKC-beta typ
C 24	12	38.7	20	20	AAZ78545	Human PKC-beta typ
C 25	12	38.7	20	20	AAZ83653	Human protein kina
C 26	12	38.7	20	20	AAZ83654	Human protein kina
C 27	12	38.7	20	20	AAZ22582	Human protein kina
C 28	12	38.7	20	20	AAZ22583	Human protein kina
C 29	12	38.7	20	20	AAZ19147	Human PKC-beta typ
C 30	12	38.7	20	20	AAZ19148	Human PKC-beta typ
C 31	12	38.7	20	21	AAA92056	Mammalian Lhx3 PCR
C 32	12	38.7	20	24	ABL90874	Human protein kina
C 33	12	38.7	20	24	ABL90875	Human protein kina
C 34	12	38.7	22	17	AAT31189	Friend virus strai
C 35	12	38.7	25	24	ABT03649	Human Lhx-3 gene p
C 36	12	38.7	28	21	AAA92110	Human Lhx3 PCR pri
C 37	12	38.7	28	21	AAA92119	Human Lhx3 PCR pri
C 38	12	38.7	33	21	AAZ12490	PCR primer used to
C 39	12	38.7	43	24	AAZ38427	Oligonucleotide pr
C 40	11	35.5	15	24	AAS98338	Galanin receptor g
C 41	11	35.5	15	24	AAS98343	Galanin receptor g
C 42	11	35.5	17	21	AAFO2170	Hammerhead ribozym
C 43	11	35.5	18	20	AAZ36966	Human cdc37 nuclei
C 44	11	35.5	19	21	AAZ2997	cdk6 ribozyme bind
C 45	11	35.5	19	22	AAH58159	Cell-cycle depende

ALIGNMENTS

RESULT 1
AA10298/c
ID AAT10298 standard; DNA; 30 BP.
XX
AC AAT10298;
XX
DT 09-SEP-1996 (first entry)
XX
DE RNA component of human telomerase antisense plasmid PCR primer G1.
XX
KW RNA component; human; telomerase; lung fibroblast; cell line WI-38;
KW recombinant production; synthesis; mutant; detection; mammalian;
KW identification; modulating agent; neoplastic condition;
KW transcriptional regulatory sequence; gene therapy; disease;
KW polymerase chain reaction; antisense plasmid; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9601835-A1.
XX
PD 25-JAN-1996.
XX
PF 06-JUL-1995; 95WO-US08530.
XX
PR 07-JUN-1995; 95US-0482115.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 07-JUN-1995; 95US-0472802.
XX
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Feng J, Funk W, Villeponteau B;

XX WPI; 1996-097581/10.
 XX RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents
 XX
 XX Example 8; Page 80; 114pp; English.
 CC The present sequence is a PCR primer for a RNA component of human
 CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
 CC genomic DNA library obtd. from the human lung fibroblast cell line
 CC WI-38. The RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene
 CC therapy of human diseases.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 11 G; 0 U; 0 other;
 Query Match 71.0%; Score 22; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCGCGCTGTTTCTC 22
 |||||
 Db 22 CTCCTCCGCGCGCTGTTTCTC 1
 RESULT 2
 AAT11043/c
 ID AAT11043 standard; DNA; 30 BP.
 AC AAT11043;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Primer for production of telomerase antisense oligonucleotide.
 XX
 KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601614-A2.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08620.
 XX
 PR 07-JUN-1995; 95US-0485778.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 13-FEB-1995; 95US-0387524.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA (GERO-) GERON CORP.
 XX
 PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhuenda MA, Villeponteau B;
 XX
 WPI; 1996-097428/10.
 XX
 XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX
 XX Example 1; Page 53; 85pp; English.

CC The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation.
 CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
 CC antisense oligonucleotides which were then used to produce antisense
 CC expression plasmids. AAT11040 was used alongside both AAT11043 and
 CC AAT11044 to produce two different antisense molecules.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 11 G; 0 U; 0 other;
 Query Match 71.0%; Score 22; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCGCGCTGTTTCTC 22
 |||||
 Db 22 CTCCTCCGCGCGCTGTTTCTC 1
 RESULT 3
 AAT11059
 ID AAT11059 standard; DNA; 30 BP.
 AC AAT11059;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Primer used for amplifying telomerase RNA fragments.
 XX
 KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601614-A2.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08620.
 XX
 PR 07-JUN-1995; 95US-0485778.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 13-FEB-1995; 95US-0387524.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA (GERO-) GERON CORP.
 XX
 PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhuenda MA, Villeponteau B;
 XX
 WPI; 1996-097428/10.
 XX
 XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX
 XX Example 15; Page 60; 85pp; English.
 CC The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the

CC telomerase gene (also claimed) can be used for study of telomere regulation in vivo, and the role it plays in immortalisation.
 CC Four primers (AAT11057, AAT11058 and AAT11059, AAT11060) which are complementary to human telomerase RNA component sequences can be used to identify and amplify homologous sequences from other CC non-human mammals. The amplified fragments can then be used as CC probes to identify telomerase genes.
 XX Sequence 30 BP; 3 A; 9 C; 7 G; 11 T; 0 other;
 SQ Query Match 67.7%; Score 21; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCGCTGTTTCTCGCTGACT 29
 Db 10 GCGCTGTTTCTCGCTGACT 30
 RESULT 4
 AAZ33130
 ID AAZ33130 standard; DNA; 22 BP.
 XX AC AAZ33130;
 XX DT 26-JAN-2000 (first entry)
 XX DE Treponema pallidum Msp variable region sense PCR primer S7.
 XX KW Treponema pallidum; syphilis; vaccine; treponemal disease; Msp;
 KW major sheath protein; bejal; gingivitis; periodontal disease; pinta;
 KW yaws; PCR primer; ss.
 XX OS Synthetic.
 OS Treponema pallidum.
 XX WO9953099-A1.
 XX PD 21-OCT-1999.
 XX PF 09-APR-1999; 99WO-US07886.
 XX PR 10-APR-1998; 98US-0058968.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Van Voorhis.WC, Lukehart SA, Centurion-Lara GA, Cameron CES;
 XX WPI; 1999-620445/53.
 XX Novel proteins useful in vaccines against syphilis and other treponemal diseases -
 Claim 3; Page 86; 200pp; English.
 The present invention describes novel Treponema pallidum genes. These genes encode a glycerophosphodiester phosphodiesterase (Gpd), a D15/Oma87 homologue, and proteins with homology to major outer sheath (Msp) proteins of T. denticola. Also described are: (1) an isolated protein capable of inducing a protective immunologic response to T. p. pallidum, T. p. pertenue, or T. p. endemicum, when administered in an effective amount to an animal host; (2) a method of identifying a T. p. pallidum vaccine candidate; (3) a method of inducing a protective immune response against T. pallidum; (4) a method for analysing a sample of DNA to determine whether it originated from T. p. subspecies pallidum, T. p. subspecies pertenue or T. p. subspecies endemicum; and (5) a method of determining whether a first and a second clinical isolate of T. p. pallidum are the same or different. The proteins are used, either alone or in combination, in vaccines against Treponemal diseases, e.g. syphilis, bejal, pinta, yaws, gingivitis, and periodontal disease. They may also provide protection against other treponemal diseases. The methods may be used to identify vaccine candidates, and to determine the origin of a treponemal nucleic acid.

CC AAZ33104 to AAZ33156, and AAY52773 to AAY52831, represent sequences used in the exemplification of the present invention.
 XX Sequence 22 BP; 1 A; 6 C; 4 G; 11 T; 0 other;
 SQ Query Match 45.2%; Score 14; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TTTTCTCGCTGAC 28
 Db 2 TTTTCTCGCTGAC 15
 RESULT 5
 AAZ07291/c
 ID AAZ07291 standard; DNA; 20 BP.
 XX AC AAZ07291;
 XX DT 22-OCT-1999 (first entry)
 XX DE Mouse telomerase RNA gene specific primer mTRr1.
 XX KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
 KW gene therapy; thymidine kinase gene; anticancer therapy; mouse;
 KW PCR primer; ss.
 XX OS Synthetic.
 OS Mus sp.
 XX WO9938964-A2.
 XX PD 05-AUG-1999.
 XX PF 29-JAN-1999; 99WO-GB00308.
 XX PR 29-JAN-1998; 98GB-0001902.
 XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX PI Keith WN;
 XX WPI; 1999-479183/40.
 XX Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy
 Disclosure; Fig 6; 109pp; English.
 The invention relates to promoter regions from mouse and human telomerase RNA (TR) component genes. The TR gene promoter can be linked to a heterologous gene, especially a gene encoding a cytotoxin, for therapy of cancer, especially neoplasia. The telomerase is necessary for the unrestricted proliferative capacity of many human cancers. Mutation or dysregulation of the telomerase repression pathway may cause reactivation or upregulation of telomerase expression in cancer. Substances, identified in the methods, can be used to block transcription from the TR gene promoter through interaction of the 5' regulatory sequences. These substances, e.g. antisense oligonucleotides, transcription factors, peptide nucleic acids and factors that disrupt signal transduction, are useful for cancer therapy. In particular, gene therapy vectors (especially pGT62-codAupp) comprising the promoter and a viral thymidine kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that neoplasia can be controlled or treated. Direct down-regulation of telomerase RNA gene through manipulation of transcription factors may be effective anticancer therapy and the cloning of the HTR gene promoter allows the analysis of therapeutic molecules which modulate HTR promoter activity. Sequences AAZ07681-95 represent PCR primers for amplifying mouse TR gene (terc) promoter sequence.
 XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

Query Match 41.9%; Score 13; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCTCGCTGACTT 30
DB 20 TTCTCGCTGACTT 8

RESULT 6
AAZ07294/c
ID AAZ07294 standard; DNA; 20 BP.

XX AC AAZ07294;

XX DT 22-OCT-1999 (first entry)

XX DE Mouse telomerase RNA gene specific primer mTR1.

XX KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
XX KW gene therapy; thymidine kinase gene; anticancer therapy; mouse;
XX KW PCR primer; ss.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO9938964-A2.

XX PD 05-AUG-1999.

XX PF 29-JAN-1999; 99WO-GB00308.

XX PR 29-JAN-1998; 98GB-0001902.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PI Keith WN;

XX DR WPI; 1999-479183/40.

XX PT Mouse and human telomerase RNA gene promoters, useful for tumor
specific gene therapy

XX PS Disclosure; Fig 6; 109pp; English.

XX CC The invention relates to promoter regions from mouse and human
telomerase RNA (TR) component genes. The TR gene promoter can be linked
to a heterologous gene, especially a gene encoding a cytotoxin, for
therapy of cancer, especially neoplasias. The telomerase is necessary for
the unrestricted proliferative capacity of many human cancers. Mutation
or dysregulation of the telomerase repression pathway may cause
reactivation or upregulation of telomerase expression in cancer.
Substances, identified in the methods, can be used to block transcription
from the TR gene promoter through interaction of the 5' regulatory
sequences. These substances, e.g. antisense oligonucleotides,
transcription factors, peptide nucleic acids and factors that disrupt
signal transduction, are useful for cancer therapy. In particular, gene
therapy vectors (especially pGT62-codAupp) comprising the promoter and a
viral thymidine kinase gene can be used to convert a prodrug, e.g.
gancyclovir, so that neoplasia can be controlled or treated. Direct
down-regulation of telomerase RNA gene through manipulation of
transcription factors may be effective anticancer therapy and the cloning
of the hTR gene promoter allows the analysis of therapeutic molecules
which modulate hTR promoter activity. Sequences AAZ07681-95 represent PCR
primers for amplifying mouse TR gene (terc) promoter sequence.

XX SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

Query Match 41.9%; Score 13; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCTCGCTGACTT 30

DB 20 TTCTCGCTGACTT 8

RESULT 7

AAA29625

ID AAA29625 standard; DNA; 22 BP.

XX AC AAA29625;

XX DT 10-AUG-2000 (first entry)

XX DE Tick derived cysteine protease primer PR-2.

XX KW Tick; vaccine; infection; salivary gland antigen; immunogen;
XX KW serine protease; cysteine protease; blood sucker; primer; ss.

XX OS Haemaphysalis longicornis.

XX PN JP2000083677-A.

XX PD 28-MAR-2000.

XX PF 17-SEP-1998; 98JP-0281932.

XX PR 17-SEP-1998; 98JP-0281932.

XX PA (FARB) BAYER KK.

XX DR WPI; 2000-296340/26.

XX PT A gene encoding tick salivary gland antigen - useful as a vaccine for
protecting animals from tick-carried infections

XX PS Example 7; Page 15; 29pp; Japanese.

XX CC The present sequence represents a primer used in the isolation of a tick
derived cysteine protease. The present invention also describes a tick
salivary gland antigen related immunogen and a tick derived serine
protease. A nucleotide sequence encoding any of the above proteins can
be used in a vaccine against tick carried infections for domestic
animals such as cattle.

XX SQ Sequence 22 BP; 3 A; 7 C; 4 G; 8 T; 0 other;

Query Match 41.9%; Score 13; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTTTTCTCG 23

DB 4 GCTGTTTTCTCG 16

RESULT 8

ABL60273/c

ID ABL60273 standard; DNA; 28 BP.

XX AC ABL60273;

XX DT 30-JUL-2002 (first entry)

XX DE Borrelia burgdorferi ZS7 ospA PCR primer 1.

XX KW Lyme disease; spirochete; antibacterial; Borrelia; infection; vaccine;
XX KW Lyme borreliosis; veterinary; PCR; primer; ospA; ss.

XX OS Borrelia burgdorferi.

XX PN DE10126367-A1.

XX PD 23-MAY-2002.

PF 30-MAY-2001; 2001DE-1026367.
 XX
 PR 20-NOV-2000; 2000DE-1057442.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Simon MM, Wallich R;
 XX
 XX WPI; 2002-445465/48.
 DR
 XX Pharmaceutical composition comprises Borrelia antigens and encoding
 PT nucleic acid, useful for diagnosis, treatment and prevention of Lyme
 PT borreliosis .
 XX
 PS Example 1; Page 6; 58pp; German.
 XX
 XX The invention relates to a pharmaceutical composition comprising at least
 CC one of: (a) a polypeptide (I) comprising fully defined sequences of
 CC ABB77511, ABB77512, ABB77514 or ABB77521 or the corresponding polypeptide
 CC from other Borrelia or their immunogenic fragments; (b) nucleic acids
 CC (II) that encode (I) or sequences that hybridise with them under
 CC stringent conditions; or (c) antibodies directed against (I). The
 CC antibodies are used for diagnosis of Borrelia infection (Lyme
 CC borreliosis) and in vaccines for Borrelia infection (Lyme
 CC borreliosis), in human or veterinary medicine. The present sequence is that
 CC of a PCR primer for amplification of a Borrelia burgdorferi
 CC polynucleotide sequence of the invention.
 XX
 SQ Sequence 28 BP; 10 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 41.9%; Score 13; DB 24; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GCTGTTTCTCG 23
 DB 28 GCTGTTTCTCG 16
 RESULT 9
 AAZ07292/c
 ID AAZ07292 standard; DNA; 29 BP.
 XX
 AC AAZ07292;
 XX
 XX 22-OCT-1999 (first entry)
 DT
 XX
 DE Mouse telomerase RNA gene specific primer mtr30r.
 XX
 KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
 KW gene therapy; thymidine kinase gene; anticancer therapy; mouse;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO938964-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JAN-1999; 99WO-GB00308.
 XX
 PR 29-JAN-1998; 98GB-0001902.
 XX
 XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA
 XX Keith WN;
 PI
 XX WPI; 1999-479183/40.
 DR
 XX Mouse and human telomerase RNA gene promoters, useful for tumor
 PT specific gene therapy
 PT
 XX

PS Disclosure; Fig 6; 109pp; English.
 XX
 CC The invention relates to promoter regions from mouse and human
 CC telomerase RNA (TR) component genes. The TR gene promoter can be linked
 CC to a heterologous gene, especially a gene encoding a cytotoxin, for
 CC therapy of cancer, especially neoplasias. The telomerase is necessary for
 CC the unrestricted proliferative capacity of many human cancers. Mutation
 CC or dysregulation of the telomerase repression pathway may cause
 CC reactivation or upregulation of telomerase expression in cancer.
 CC Substances, identified in the methods, can be used to block transcription
 CC from the TR gene promoter through interaction of the 5' regulatory
 CC sequences. These substances, e.g. antisense oligonucleotides,
 CC transcription factors, peptide nucleic acids and factors that disrupt
 CC signal transduction, are useful for cancer therapy. In particular, gene
 CC therapy vectors (especially pGT62-codAupp) comprising the promoter and a
 CC viral thymidine kinase gene can be used to convert a prodrug, e.g.
 CC gancyclovir, so that neoplasia can be controlled or treated. Direct
 CC down-regulation of telomerase RNA gene through manipulation of
 CC transcription factors may be effective anticancer therapy and the cloning
 CC of the HTR gene promoter allows the analysis of therapeutic molecules
 CC which modulate HTR promoter activity. Sequences AAZ07681-95 represent PCR
 CC primers for amplifying mouse TR gene (terc) promoter sequence.
 XX
 SQ Sequence 29 BP; 8 A; 8 C; 9 G; 4 T; 0 other;
 Query Match 41.9%; Score 13; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 TTTCGCTGACTT 30
 DB 29 TTTCGCTGACTT 17
 RESULT 10
 AAS98334/c
 ID AAS98334 standard; DNA; 15 BP.
 XX
 AC AAS98334;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX
 DE Galanin receptor gene GALR1 allele-specific oligonucleotide #46.
 XX
 KW Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;
 KW drug discovery; haplotyping; infectious diarrhoea;
 KW growth hormone deficiency; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179237-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US12306.
 XX
 PR 14-APR-2000; 2000US-197838P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
 PI
 XX WPI; 2002-066341/09.
 DR
 XX Genotyping human galanin receptor gene of an individual for determining
 PT haplotype of an individual, involves determining the identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the
 PT gene -
 XX
 PS Claim 16; Page 15; 99pp; English.
 XX
 CC The invention relates to genotyping human galanin receptor (GALR1) gene
 CC of an individual, involving determining for the two copies of the GALR1

CC gene present in the individual, the identity of the nucleotide pair at
 CC one or more polymorphic sites. The method is useful for determining
 CC whether an individual has a haplotype or haplotype pairs defined in the
 CC specification. This is useful for improving the efficacy and reliability
 CC of several steps in the discovery and development of drugs for treating
 CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
 CC growth hormone deficiency, to validate GALR1 as a candidate agent for
 CC treating a specific condition or disease predicted to be associated with
 CC GALR1 activity, and in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease predicted to be associated
 CC with GALR1 activity. The method is useful to screen for compounds
 CC targeting GALR1 to treat a specific condition or disease associated
 CC with GALR1 activity. A GALR1 polynucleotide or variant is useful in
 CC studying the expression and function of GALR1, and in expressing GALR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to GALR1 activity. The polynucleotide or variant is useful for
 CC studying expression of the GALR1 isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against GALR1 protein, and for studying the
 CC effect of the variation on the biological activity of GALR1 as well as on
 CC the binding affinity of candidate drugs targeting GALR1 for the treatment
 CC of infectious diarrhoea and growth hormone insufficiency. AAS98289-
 CC AAS98408 represent human GALR1 gene allele-specific oligonucleotides used
 CC to detect GALR1 gene polymorphisms as described in the method of the
 CC invention.
 XX

SQ Sequence 15 BP; 2 A; 3 C; 9 G; 0 U; 1 other;

Query Match 38.7%; Score 12; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 |||||
 Db 12 CTCCTCCGCGCGC 1

RESULT 11

AAS98336/c
 ID AAS98336 standard; DNA; 15 BP.

AC AAS98336;

XX 12-MAR-2002 (first entry)

XX Galanin receptor gene GALR1 allele-specific oligonucleotide #48.

XX Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;

KW drug discovery; haplotyping; infectious diarrhoea;

KW growth hormone deficiency; allele-specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200179237-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US12306.

XX 14-APR-2000; 2000US-197838P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;

XX WPI; 2002-066341/09.

XX Genotyping human galanin receptor gene of an individual for determining

PT haplotype of an individual, involves determining the identity of

PT nucleotide pair at specific polymorphic sites for two copies of the

PT gene

XX Claim 16; Page 15; 99pp; English.

XX

CC The invention relates to genotyping human galanin receptor (GALR1) gene
 CC of an individual, involving determining for the two copies of the GALR1
 CC gene present in the individual, the identity of the nucleotide pair at
 CC one or more polymorphic sites. The method is useful for determining
 CC whether an individual has a haplotype or haplotype pairs defined in the
 CC specification. This is useful for improving the efficacy and reliability
 CC of several steps in the discovery and development of drugs for treating
 CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
 CC growth hormone deficiency, to validate GALR1 as a candidate agent for
 CC treating a specific condition or disease predicted to be associated with
 CC GALR1 activity, and in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease predicted to be associated
 CC with GALR1 activity. The method is useful to screen for compounds
 CC targeting GALR1 to treat a specific condition or disease associated
 CC with GALR1 activity. A GALR1 polynucleotide or variant is useful in
 CC studying the expression and function of GALR1, and in expressing GALR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to GALR1 activity. The polynucleotide or variant is useful for
 CC studying expression of the GALR1 isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against GALR1 protein, and for studying the
 CC effect of the variation on the biological activity of GALR1 as well as on
 CC the binding affinity of candidate drugs targeting GALR1 for the treatment
 CC of infectious diarrhoea and growth hormone insufficiency. AAS98289-
 CC AAS98408 represent human GALR1 gene allele-specific oligonucleotides used
 CC to detect GALR1 gene polymorphisms as described in the method of the
 CC invention.
 XX

SQ Sequence 15 BP; 1 A; 3 C; 10 G; 0 U; 1 other;

Query Match 38.7%; Score 12; DB 24; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 |||||
 Db 13 CTCCTCCGCGCGC 2

RESULT 12

AAS98341

ID AAS98341 standard; DNA; 15 BP.

XX AAS98341;

XX 12-MAR-2002 (first entry)

XX Galanin receptor gene GALR1 allele-specific oligonucleotide #53.

XX Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;

KW drug discovery; haplotyping; infectious diarrhoea;

KW growth hormone deficiency; allele-specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200179237-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US12306.

XX 14-APR-2000; 2000US-197838P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;

XX WPI; 2002-066341/09.

XX Genotyping human galanin receptor gene of an individual for determining

PT haplotype of an individual, involves determining the identity of

PT nucleotide pair at specific polymorphic sites for two copies of the

PT gene

XX

PS Claim 16; Page 15; 99pp; English.

XX The invention relates to genotyping human galanin receptor (GALR1) gene
CC of an individual, involving determining for the two copies of the GALR1
CC gene present in the individual, the identity of the nucleotide pair at
CC one or more polymorphic sites. The method is useful for determining
CC whether an individual has a haplotype or haplotype pairs defined in the
CC specification. This is useful for improving the efficacy and reliability
CC of several steps in the discovery and development of drugs for treating
CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
CC growth hormone deficiency, to validate GALR1 as a candidate agent for
CC treating a specific condition or disease predicted to be associated with
CC GALR1 activity, and in the design of clinical trials of candidate drugs
CC for treating a specific condition or disease predicted to be associated
CC with GALR1 activity. The method is useful to screen for compounds
CC targeting GALR1 to treat a specific condition or disease associated
CC with GALR1 activity. A GALR1 polynucleotide or variant is useful in
CC studying the expression and function of GALR1, and in expressing GALR1
CC protein for use in screening for candidate drugs to treat diseases
CC related to GALR1 activity. The polynucleotide or variant is useful for
CC studying expression of the GALR1 isogenes in vivo, for in vivo screening
CC and testing of drugs targeted against GALR1 protein, and for studying the
CC effect of the variation on the biological activity of GALR1 as well as on
CC the binding affinity of candidate drugs targeting GALR1 for the treatment
CC of infectious diarrhoea and growth hormone insufficiency. AAS98289-
CC AAS98408 represent human GALR1 gene allele-specific oligonucleotides used
CC to detect GALR1 gene polymorphisms as described in the method of the
CC invention.

SQ Sequence 15 BP; 0 A; 10 C; 3 G; 1 T; 1 other;

Query Match 38.7%; Score 12; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
|||
DB 2 CTCCTCCGCGCGC 13

RESULT 13
AAQ49677/c
ID AAQ49677 standard; DNA; 20 BP.

XX AAQ49677;

XX 25-APR-1994 (first entry)

DE PKC-beta type I and II translation initiation codon binding
oligomer 139-120.

XX Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
KW phosphorothionate linkage; PKC; transcription initiation site;
KW translation initiation site; 5' cap region; intron/exon boundary;
KW diagnosis; therapeutics; prophylaxis; ss.

XX Synthetic.

XX Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a

FT /note= "Phosphorothionate linkages"

XX WO9319203-A.

XX 30-SEP-1993.

XX 25-FEB-1993; 93WO-US02213.

XX 16-MAR-1992; 92US-0852852.

XX (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Dean N;
XX WPI; 1993-320768/40.

XX Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein
PT kinase C - useful as diagnostics and therapeutics for disease
PT states associated with particular isozymes of PKC

XX Claim 6; Page 18; 64pp; English.

XX The sequences given in AAQ49657-707 are antisense oligonucleotides
CC which contain altered inter-sugar linkages, pref. phosphorothionate
CC linkages. These oligomers bind with the protein kinase C (PKC) mRNA
CC at the transcription initiation site, the translation initiation
CC site, the 5' cap region, an intron/exon boundary, coding sequences
CC or sequences in the 5'- or 3'-untranslated regions. These
CC oligonucleotides may be used in diagnostics, therapeutics,
CC prophylaxis and as research reagents. The numbers allocated to
CC the oligonucleotides are relative to the first residue to be sequenced
CC on the cDNA, which is 28 residues upstream of the ATG start codon.

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 38.7%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
|||
DB 18 CTCCTCCGCGCGC 7

RESULT 14
AAQ49678/c
ID AAQ49678 standard; DNA; 20 BP.

XX AAQ49678;

XX 25-APR-1994 (first entry)

DE PKC-beta type I and II translation initiation codon binding
oligomer 134-115.

XX Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
KW phosphorothionate linkage; PKC; transcription initiation site;
KW translation initiation site; 5' cap region; intron/exon boundary;
KW diagnosis; therapeutics; prophylaxis; ss.

XX Synthetic.

XX Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a

FT /note= "Phosphorothionate linkages"

XX WO9319203-A.

XX 30-SEP-1993.

XX 25-FEB-1993; 93WO-US02213.

XX 16-MAR-1992; 92US-0852852.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean N;

XX WPI; 1993-320768/40.

XX Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein
PT kinase C - useful as diagnostics and therapeutics for disease
PT states associated with particular isozymes of PKC

XX

PS Claim 6; Page 18; 64pp; English.

XX The sequences given in AAQ49657-707 are antisense oligonucleotides

CC which contain altered inter-sugar linkages, pref. phosphorothionate

CC linkages. These oligomers bind with the protein kinase C (PKC) mRNA

CC at the transcription initiation site, the translation initiation

CC site, the 5' cap region, an intron/exon boundary, coding sequences

CC or sequences in the 5'- or 3'-untranslated regions. These

CC oligonucleotides may be used in diagnostics, therapeutics,

CC prophylaxis and as research reagents. The numbers allocated to

CC the oligonucleotides are relative to the first residue to be sequenced

CC on the cDNA, which is 28 residues upstream of the AUG start codon.

XX

SQ Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 other;

Query Match 38.7%; Score 12; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12

DB 13 CTCCTCCGCGCGC 2

RESULT 15

AAQ97894/c

ID AAQ97894 standard; DNA; 20 BP.

XX

AC AAQ97894;

XX

DT 17-OCT-1995 (first entry)

XX

DE PNA oligomer targetting AUG region of PKC-beta isoforms I & II.

XX

KW Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;

KW cell proliferation; cell differentiation; isozyme; antisense;

KW triple helix; cancer; psoriasis; inflammation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_feature 1..20

FT /tag= a

FT /note= "at least one (and preferably all) of

FT the backbone subunits are composed of N-acetyl

FT N-(2-aminoethyl)glycine peptide residues, the

FT nucleobase being attached covalently to the

FT acetyl group and the peptide linkage being

FT formed by condensation of the glycine

FT carboxy group of one residue with the amino

FT group of the 2-aminoethyl moiety in the next

FT residue"

XX

PN WO9503833-A.

XX

XX

PD 09-FEB-1995.

XX

XX

PP 28-JUL-1994; 94WO-US08465.

XX

XX

PR 29-JUL-1993; 93US-0099098.

XX

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Dean NM;

XX

XX

DR WPI; 1995-082040/11.

XX

XX

PT New peptide nucleic acid oligomers specific for protein kinase C

PT isozyme(s) - useful as anti-sense molecules for treating PKC

PT mediated disease, e.g. cancer, psoriasis and inflammation

XX

XX

XX Claim 10; Page 261; 287pp; English.

XX

CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist

CC of naturally occurring nucleobases covalently bound to a polyamide

CC backbone and (b) hybridise to the translation initiation AUG region,

CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region

CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target

CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene

CC regulation moieties. They inhibit expression of PKC-alpha and its

CC isoforms (including beta, gamma, delta, epsilon, zeta and eta) and so

CC are useful for treating and diagnosing cell proliferation and

CC differentiation processes such as neoplastic, hyperproliferative

CC and inflammatory diseases.

CC PNA oligomers have high affinity for complementary single stranded DNA.

CC They are also able to form triple helices in which a first PNA strand

CC binds with RNA or ssDNA and a second PNA strand binds with the resulting

CC double helix or with the first PNA strand. The PNAs possess no

CC significant charge and are water soluble, which facilitates cellular

CC uptake. Further, since they contain amides of non-biological amino acids,

CC they are biostable and resistant to enzymatic degradation by proteases.

CC The present sequence targets the AUG region of PKC-beta isoforms I & II.

XX

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 38.7%; Score 12; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12

DB 18 CTCCTCCGCGCGC 7

Search completed: June 23, 2003, 20:09:19

Job time : 118.339 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:17:23 ; Search time 308.975 Seconds
(without alignments)
2919.933 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTTCGCTGACTTT 31

Scoring table:
Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sta.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
- 35: em_hgt_rod.*
- 36: em_hgt_man.*
- 37: em_hgt_vrt.*
- 38: em_sy.*
- 39: em_hgt_hum.*
- 40: em_hgt_mus.*
- 41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	22	71.0	30	6	AR016054	AR016054 Sequence
C 2	22	71.0	30	6	AR059215	AR059215 Sequence
C 3	22	71.0	30	6	AR075526	AR075526 Sequence
C 4	22	71.0	30	6	AR161924	AR161924 Sequence
C 5	22	71.0	30	6	I31769	I31769 Sequence
C 6	21	67.7	28	6	AR016060	AR016060 Sequence
C 7	21	67.7	28	6	AR075532	AR075532 Sequence
C 8	13	41.9	20	6	AX019577	AX019577 Sequence
C 9	13	41.9	20	6	AX019580	AX019580 Sequence
C 10	13	41.9	29	6	AX019578	AX019578 Sequence
C 11	12	38.7	20	6	AR076656	AR076656 Sequence
C 12	12	38.7	20	6	AR076657	AR076657 Sequence
C 13	12	38.7	20	6	AR182713	AR182713 Sequence
C 14	12	38.7	20	6	AR182714	AR182714 Sequence
C 15	12	38.7	20	6	AX226311	AX226311 Sequence
C 16	12	38.7	20	6	AX226312	AX226312 Sequence
C 17	12	38.7	20	6	I87125	I87125 Sequence
C 18	12	38.7	20	6	I87126	I87126 Sequence
C 19	12	38.7	22	6	A51391	A51391 Sequence
C 20	12	38.7	25	6	E16661	E16661 PCR primer
C 21	11	35.5	18	6	A97274	A97274 Sequence
C 22	11	35.5	19	6	AX129365	AX129365 Sequence
C 23	11	35.5	20	6	AR122485	AR122485 Sequence
C 24	11	35.5	20	6	AR124806	AR124806 Sequence
C 25	11	35.5	20	6	AR161568	AR161568 Sequence
C 26	11	35.5	20	6	AX298535	AX298535 Sequence
C 27	11	35.5	20	6	I89927	I89927 Sequence
C 28	11	35.5	21	12	AB068319	AB068319 Synthetic
C 29	11	35.5	25	6	AX350093	AX350093 Sequence
C 30	11	35.5	27	6	AR039910	AR039910 Sequence
C 31	11	35.5	27	6	AR184928	AR184928 Sequence
C 32	11	35.5	27	6	AR191109	AR191109 Sequence
C 33	11	35.5	27	6	AR191441	AR191441 Sequence
C 34	11	35.5	29	6	A49464	A49464 Sequence
C 35	11	35.5	29	6	AR093964	AR093964 Sequence
C 36	11	35.5	30	6	AR037771	AR037771 Sequence
C 37	11	35.5	30	6	I17308	I17308 Sequence
C 38	11	35.5	31	6	A23777	A23777 CASOL10 oli
C 39	11	35.5	31	6	I47763	I47763 Sequence
C 40	11	35.5	35	6	AX181212	AX181212 Sequence
C 41	11	35.5	40	6	AR053660	AR053660 Sequence
C 42	11	35.5	40	6	AR053705	AR053705 Sequence
C 43	11	35.5	40	6	AR054939	AR054939 Sequence
C 44	11	35.5	40	6	AR093969	AR093969 Sequence
C 45	11	35.5	40	6	AR175941	AR175941 Sequence

ALIGNMENTS

RESULT 1	AR016054/c	AR016054	30 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	Sequence 22 from patent US 5776679.					
DEFINITION						
ACCESSION	AR016054					
VERSION	AR016054.1	GI:3972331				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 30)					
AUTHORS	Villeponteau B., Feng, J., Funk, W. and Andrews, W.H.					
TITLE	Assays for the DNA component of human telomerase					
JOURNAL	Patent: US 5776679-A 22 07-JUL-1998;					
FEATURES	Location/Qualifiers					

```
source
1. .30
/organism="unknown"
BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGGCGGCTGTTTCTC 22
Db 22 CTCCTCCGGCGGCTGTTTCTC 1

RESULT 2
AR059215/c
LOCUS AR059215 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5837857.
ACCESSION AR059215
VERSION AR059215.1 GI:5984792
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 22 17-NOV-1998;
FEATURES
Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGGCGGCTGTTTCTC 22
Db 22 CTCCTCCGGCGGCTGTTTCTC 1

RESULT 3
AR075526/c
LOCUS AR075526 30 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 23 from patent US 5958680.
ACCESSION AR075526
VERSION AR075526.1 GI:10002274
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 23 28-SEP-1999;
FEATURES
Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGGCGGCTGTTTCTC 22
Db 22 CTCCTCCGGCGGCTGTTTCTC 1

RESULT 4
AR059215/c
LOCUS AR059215 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5837857.
ACCESSION AR059215
VERSION AR059215.1 GI:5984792
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 22 17-NOV-1998;
FEATURES
Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGGCGGCTGTTTCTC 22
Db 22 CTCCTCCGGCGGCTGTTTCTC 1

RESULT 5
AR075526/c
LOCUS AR075526 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 22 from patent US 5583016.
ACCESSION AR075526
VERSION AR075526.1 GI:1822560
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5583016-A 22 10-DEC-1996;
FEATURES
Location/Qualifiers
1. .30
/organism="unknown"
BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGGCGGCTGTTTCTC 22
Db 22 CTCCTCCGGCGGCTGTTTCTC 1

RESULT 6
AR016060/c
LOCUS AR016060 28 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 28 from patent US 5776679.
ACCESSION AR016060
VERSION AR016060.1 GI:3972337
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 28 07-JUL-1998;
FEATURES
Location/Qualifiers
1. .28
source
```

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BASE COUNT      12 a      6 c      10 g      0 t
ORIGIN

Query Match      67.7%; Score 21; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 7
AR075532/c
LOCUS      AR075532      28 bp      DNA      linear      PAT 30-AUG-2000
DEFINITION Sequence 29 from patent US 5958680.
ACCESSION  AR075532
VERSION     AR075532.1 GI:10002280
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE      Mammalian telomerase
JOURNAL    Patent: US 5958680-A 29 28-SEP-1999;
FEATURES   Location/Qualifiers
            source
            1..28
            /organism="unknown"
BASE COUNT   12 a      6 c      10 g      0 t
ORIGIN

Query Match      67.7%; Score 21; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 8
AR019577/c
LOCUS      AR019577      20 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 31 from Patent WO9938964.
ACCESSION  AR019577
VERSION     AR019577.1 GI:10043491
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Keith, W.N.
TITLE      Promoter regions of the mouse and human telomerase rna component
JOURNAL    Patent: WO 9938964-A 31 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="primer"
BASE COUNT   6 a      5 c      7 g      2 t
ORIGIN

Query Match      41.9%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 20 TTCTCGCTGACTT 8

RESULT 9
AR019580/c
LOCUS      AR019580      20 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 34 from Patent WO9938964.
ACCESSION  AR019580
VERSION     AR019580.1 GI:10043494
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Keith, W.N.
TITLE      Promoter regions of the mouse and human telomerase rna component
JOURNAL    Patent: WO 9938964-A 34 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="primer"
BASE COUNT   6 a      5 c      7 g      2 t
ORIGIN

Query Match      41.9%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 20 TTCTCGCTGACTT 8

RESULT 10
AR019578/c
LOCUS      AR019578      29 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 32 from Patent WO9938964.
ACCESSION  AR019578
VERSION     AR019578.1 GI:10043492
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Keith, W.N.
TITLE      Promoter regions of the mouse and human telomerase rna component
JOURNAL    Patent: WO 9938964-A 32 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES   Location/Qualifiers
            source
            1..29
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="primer"
BASE COUNT   8 a      8 c      9 g      4 t
ORIGIN

Query Match      41.9%; Score 13; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 29 TTCTCGCTGACTT 17

RESULT 11
AR076656/c
LOCUS      AR076656      20 bp      DNA      linear      PAT 30-AUG-2000
DEFINITION Sequence 21 from patent US 5959096.
ACCESSION  AR076656
```

```
VERSION AR076656.1 GI:10003402
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 21 28-SEP-1999;
FEATURES
    source
    1..20
    /organism="unknown"
BASE COUNT 2 a 7 c 8 g 3 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 18 CTCCTCCGCGCGC 7

RESULT 12
LOCUS AR076657/c
DEFINITION Sequence 22 from patent US 5959096.
ACCESSION AR076657
VERSION AR076657.1 GI:10003403
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 22 28-SEP-1999;
FEATURES
    source
    1..20
    /organism="unknown"
BASE COUNT 2 a 6 c 11 g 1 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 18 CTCCTCCGCGCGC 7

RESULT 13
LOCUS AR182713/c
DEFINITION Sequence 21 from patent US 6339066.
ACCESSION AR182713
VERSION AR182713.1 GI:20225920
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of high chiral purity and which modulate .beta.I., .beta.II., .gamma., .delta., .EPSILON., .zeta. and .eta. isoforms of human protein kinase C
JOURNAL Patent: US 6339066-A 21 15-JAN-2002;
FEATURES
    source
    1..20
    /organism="unknown"
BASE COUNT 2 a 7 c 8 g 3 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 13 CTCCTCCGCGCGC 2

RESULT 14
LOCUS AR182714/c
DEFINITION Sequence 22 from patent US 6339066.
ACCESSION AR182714
VERSION AR182714.1 GI:20225921
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of high chiral purity and which modulate .beta.I., .beta.II., .gamma., .delta., .EPSILON., .zeta. and .eta. isoforms of human protein kinase C
JOURNAL Patent: US 6339066-A 22 15-JAN-2002;
FEATURES
    source
    1..20
    /organism="unknown"
BASE COUNT 2 a 6 c 11 g 1 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 13 CTCCTCCGCGCGC 2

RESULT 15
LOCUS AX226311/c
DEFINITION Sequence 21 from Patent EP1126025.
ACCESSION AX226311
VERSION AX226311.1 GI:15555575
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Dean,N.
TITLE Oligonucleotide modulation of protein kinase c
JOURNAL Patent: EP 1126025-A 21 22-AUG-2001;
FEATURES
    source
    1..20
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="Artificial"
BASE COUNT 2 a 7 c 8 g 3 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 13 CTCCTCCGCGCGC 12
```

RESULT 9
 AZ332622/c
 LOCUS
 DEFINITION
 35 bp DNA linear GSS 29-SBP-2000
 1M0061M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0061M11 F, DNA sequence.
 ACCESSION
 AZ332622
 VERSION
 AZ332622.1 GI:10396450
 KEYWORDS
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 35)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D.,Weiss,R.
 TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 5177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0061 row: M column: 11
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 35.
 Location/Qualifiers
 1..35
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0061M11"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI14732114|95|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

BASE COUNT 9 a 5 c 11 g 10 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GGCCATTTTTT 19
 |||||
 Db 15 GGCCATTTTTT 5

RESULT 10
 AL764814/c
 LOCUS
 DEFINITION
 40 bp DNA linear GSS 18-JUN-2002
 Arabidopsis thaliana T-DNA flanking sequence GK-131C11-012721,
 genomic survey sequence.
 ACCESSION
 AL764814
 VERSION
 AL764814.1 GI:21517857
 KEYWORDS
 GSS.
 SOURCE
 thale cress.
 ORGANISM
 Arabidopsis thaliana
 Arabidopsi
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1
 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
 and Weisshaar,B.
 TITLE
 A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 JOURNAL
 Unpublished
 COMMENT
 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 40)
 Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
 Direct Submission
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone MFJ20. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

Location/Qualifiers
 1..40
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-131C11-012721"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA from
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"
 BASE COUNT 15 a 5 c 11 g 8 t 1 others
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 ATTTTGTGCT 23
 |||||
 Db 21 ATTTTGTGCT 11
 RESULT 11
 AI266869
 LOCUS
 DEFINITION
 43 bp mRNA linear EST 16-NOV-1998
 uJ08a10.x1 Sugano mouse liver mlta Mus musculus cDNA clone
 IMAGE:1891290 3' similar to SW:ATP6_MOUSE P00848 ATP SYNTHASE A
 CHAIN:,, mRNA sequence.
 ACCESSION
 AI266869
 VERSION
 AI266869.1 GI:3885027

```

KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 43)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:975614

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1891290"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGG); Site 2: DraIII (CACCATGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCCACTGG), digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGACACA."
BASE COUNT 15 a 7 c 10 g 11 t
ORIGIN
Query Match 36.7%; Score 11; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGT 21
|||||
Db 6 CCATTTTGT 16

RESULT 12
BH813805 45 bp DNA linear GSS 02-MAY-2002
LOCUS SALK_065322 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_065322, DNA sequence.
ACCESSION BH813805
VERSION BH813805.1 GI:20392724
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
1 (bases 1 to 43)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 45
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_065322"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 7 a 5 c 12 g 21 t
ORIGIN
Query Match 36.7%; Score 11; DB 17; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGTGGTGCCA 13
|||||
Db 28 GGTGGTGCCA 38

RESULT 13
AI680115/c 46 bp mRNA linear EST 15-DEC-1999
LOCUS tw65a03.x1 NCI CGAP ut3 Homo sapiens cDNA clone IMAGE:224524.3,
DEFINITION similar to TR:000405 000405 FB19 PROTEIN. ;contains MER22.b3 MSRI
repetitive element ;, mRNA sequence.
ACCESSION AI680115
VERSION AI680115.1 GI:4890297
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

Db 18 CTCCTCCGCGCGC 7

Search completed: June 23, 2003, 20:29:43
Job time : 310.975 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 785.207 Seconds
(without alignments)
618.773 Million cell updates/sec

Title: US-08-770-564A-1_COPY_290_319

Perfect score: 30

Sequence: 1 GGGGGTGGGCCATTTTGTCTAACCCCTA 30

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	46.7	42	10 AV832474	AV832474 AV832474
C 2	13	43.3	37	9 AI862676	AI862676 wj27f04.x
C 3	11	36.7	19	17 A2514722	A2514722 IM0361C10
C 4	11	36.7	30	2 HSM001897	AI037566 Homo sapi
C 5	11	36.7	31	9 AI189788	AI189788 qc33c03.x
C 6	11	36.7	33	17 AL756125	AL756125 Arabidops

C 7	11	36.7	34	9 AA911862	AA911862 og21a09.s
C 8	11	36.7	34	9 AI623585	AI623585 ts37f06.x
C 9	11	36.7	35	17 AZ332622	AZ332622 IM0061M11
C 10	11	36.7	40	17 AL764814	AL764814 Arabidops
C 11	11	36.7	43	9 AI266869	AI266869 wj08a10.x
C 12	11	36.7	45	17 BH813805	BH813805 SALM_0853
C 13	11	36.7	46	9 AI680115	AI680115 tw65a03.x
C 14	11	36.7	46	17 AZ404140	AZ404140 IM0172J15
C 15	11	36.7	50	9 AU105989	AU105989 AU105989
C 16	11	36.7	50	9 AA257872	AA257872 MBL2S34F5
C 17	10	33.3	18	17 AZ924200	AZ924200 4905.ic27
C 18	10	33.3	19	9 AA909236	AA909236 ol08a11.s
C 19	10	33.3	23	17 AZ329120	AZ329120 IM0053A14
C 20	10	33.3	23	17 AZ481914	AZ481914 IM0306K03
C 21	10	33.3	24	17 AZ333171	AZ333171 IM0062B08
C 22	10	33.3	25	9 AA912548	AA912548 ol36c01.s
C 23	10	33.3	25	9 AL048782	AL048782 DKFZp5660
C 24	10	33.3	25	17 AZ873581	AZ873581 2M0187G19
C 25	10	33.3	26	10 AW698828	AW698828 r435 non-
C 26	10	33.3	28	9 AI377008	AI377008 tc34h10.x
C 27	10	33.3	28	9 AI635476	AI635476 ts65a03.x
C 28	10	33.3	28	17 AZ456389	AZ456389 IM0259B23
C 29	10	33.3	28	17 AZ591734	AZ591734 IM0402D05
C 30	10	33.3	28	17 AZ640640	AZ640640 IM0502H13
C 31	10	33.3	29	17 AZ308439	AZ308439 IM0011I20
C 32	10	33.3	29	17 AZ800642	AZ800642 2M0058G16
C 33	10	33.3	31	2 HSM003598	AI039122 Homo sapi
C 34	10	33.3	31	9 AI004906	AI004906 ou59a11.x
C 35	10	33.3	31	9 AI200650	AI200650 qf9a11.x
C 36	10	33.3	31	9 AI364767	AI364767 qm18d02.x
C 37	10	33.3	31	17 AZ464939	AZ464939 IM0274L06
C 38	10	33.3	32	10 AV962684	AV962684 AV962684
C 39	10	33.3	32	17 AZ471070	AZ471070 IM0285A02
C 40	10	33.3	32	17 DR9H23S	AL743393 Danio rer
C 41	10	33.3	34	9 AA861409	AA861409 ak34a12.s
C 42	10	33.3	34	9 AI149355	AI149355 qc82b03.x
C 43	10	33.3	34	9 AU013748	AU013748 AU013748
C 44	10	33.3	34	9 AU256767	AU256767 AU256767
C 45	10	33.3	34	13 BJ077096	BJ077096 BJ077096

ALIGNMENTS

RESULT 1	AV832474/c	AV832474	42 bp	mRNA	linear	EST 22-JUN-2001
LOCUS	AV832474	K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare leaves vegetative stage				
DEFINITION		clone baak3h01, mRNA sequence.				
ACCESSION	AV832474	AV832474.1	GI:14524563			
VERSION		EST.				
KEYWORDS		Hordeum vulgare subsp. vulgare.				
SOURCE		Hordeum vulgare subsp. vulgare				
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.				
REFERENCE		1 (bases 1 to 42)				
AUTHORS		Sato, K.				
TITLE		Barley EST sequencing project in NIG and Okayama Univ				
JOURNAL		Unpublished (2001)				
COMMENT		Contact: Kazuhiro Sato Research Institute for Bioresources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kzsato@rib.okayama-u.ac.jp, URL: http://www.rib.okayama-u.ac.jp/barley/ Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission; database: http://www.shigen.nig.ac.jp/barley/Barley.html.				

FEATURES

Location/Qualifiers
1..42
source

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/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112503"
/clone="baak3h01"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
16 a 6 c 5 g 14 t 1 others
BASE COUNT
ORIGIN

Query Match 46.7%; Score 14; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CATTCTTTGCTTAA 25
|||||
Db 35 CATTCTTTGCTTAA 22

RESULT 2
AI862676
LOCUS
DEFINITION
AI862676 37 bp mRNA linear EST 21-DEC-1999
wJ27f04.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404063 3'
similar to SW:TENS_CHICK Q04205 TENSIN.1, mRNA sequence.
ACCESSION
AI862676
VERSION
AI862676.1 GI:5526783
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 970 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2404063"
/clone_lib="NCI CGAP Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/notes="Organ: Kidney; Vector: pTT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."
4 a 14 c 15 g 4 t
BASE COUNT
ORIGIN

/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112503"
/clone="baak3h01"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
16 a 6 c 5 g 14 t 1 others
BASE COUNT
ORIGIN

Query Match 43.3%; Score 13; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGCCA 13
|||||
Db 24 GGGGTGGTGGCCA 36

RESULT 3
AZ514722
LOCUS
DEFINITION
AZ514722 19 bp DNA linear GSS 05-OCT-2000
1M0361C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0361C10 R, DNA sequence.
ACCESSION
AZ514722
VERSION
AZ514722.1 GI:10696038
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: C column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361C10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI:473211419b/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
3 a 4 c 4 g 8 t
BASE COUNT
ORIGIN

```

```

Query Match      36.7%; Score 11; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TGGCCATTTT 18
DB      7 TGGCCATTTT 17

RESULT 4
HSM001897/c
ID HSM001897 standard; RNA; EST; 30 BP.
XX
AC AL037566;
XX
SV AL037566.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZP564I1472_r1 (from clone DKFZP564I1472)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-30
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No si sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key
FH Location/Qualifiers
FT source
FT 1..30
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZP564I1472"
FT /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 30 BP; 22 A; 2 C; 4 G; 1 T; 1 other;

Query Match      36.7%; Score 11; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TTTTGTCTA 24
DB      18 TTTTGTCTA 8

RESULT 5
AI189788/c
LOCUS      31 bp mRNA linear EST 28-OCT-1998
DEFINITION g333403.x1 Soares_placenta_8to9weeks_2NHP8to9W Homo sapiens cDNA
            clone IMAGE:1725509 3' similar to SW:PRP2 HUMAN P02812 SALIVARY
            PROLINE-RICH PROTEIN PRECURSOR ; contains element TAR1 repetitive
            element ;, mRNA sequence.
ACCESSION      AI189788
VERSION      AI189788.1 GI:3740997

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```

KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 31)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Tumor Gene Index
        Unpublished (1997)
        Contact: Robert Strausberg, Ph.D.
        Email: cgaps-remail.nih.gov
        This clone is available royalty-free through LNL; contact the
        IMAGE Consortium (info@image.lnl.gov) for further information.
        Trace considered overall poor quality
        Insert Length: 977 Std Error: 0.00
        Seg primer: -40UP from Gibco
        High quality sequence stop: 1.
        Location/Qualifiers
            1..31
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1725509"
            /clone_lib="Soares_placenta_8to9weeks_2NHP8to9W"
            /dev_stage="two placentae: one from 8 weeks and another
            from 9 weeks post conception"
            /lab_host="DH10B (ampicillin resistant)"
            /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
            modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTACCAATCTGAAGTGGAGCGCCGCGATTTTATTTTITTTT 3'],
            double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of a modified pT7T3 vector
            (Pharmacia). Library constructed by Bento Soares and
            M. Fatima Bonaldo."
            12 a 12 c 6 g 1 t

BASE COUNT      12 a 12 c 6 g 1 t
ORIGIN
Query Match      36.7%; Score 11; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCCATTTT 19
DB      14 GGCCATTTT 4

RESULT 6
AL756125
LOCUS      33 bp DNA linear GSS 17-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-105G12-012137,
            genomic survey sequence.
ACCESSION      AL756125
VERSION      AL756125.1 GI:21488623
KEYWORDS      GSS.
SOURCE      Arabidopsis thaliana
            thale cress.
ORGANISM      Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1
            Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
            and Weissehaar,B.
            A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
            Unpublished
            2
            Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissehaar,B.
            A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
            Unpublished

```

```

REFERENCE
AUTHORS Strizhov,N., Li,Y., Rosso,M. and Weishaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone T8B10. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1. .33
Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-105G12-012137"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequences were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 6 a 6 c 5 g 16 t
ORIGIN
Query Match 36.7%; Score 11; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTTTGTCTCA 24
|||||
Db 13 TTTTGTCTCA 23

RESULT 7
AA911862/c 34 bp mRNA linear EST 21-APR-1998
LOCUS og21a09.s1 NCI CGAP PMS1 Homo sapiens cDNA clone IMAGE:1440472 3'
DEFINITION similar to TR:Q39865 Q39865 HYDROXYPROLINE-RICH GLYCOPROTEIN
:contains element MER30 repetitive element ;, mRNA sequence.
ACCESSION AA911862
VERSION AA911862.1 GI:3051254
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
/db_xref="taxon:9606"
/clone="IMAGE:1440472"
/clone_lib="NCI CGAP PMS1"
/tissue_type="dorsal root ganglion"
/lab_host="DH10B"

REFERENCE
AUTHORS NCI CGAP PMS1 Homo sapiens cDNA clone IMAGE:1440472 3'
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL Tumor Gene Index
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
Insert Length: 1082 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .34
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1440472"
/clone_lib="NCI CGAP PMS1"
/tissue_type="dorsal root ganglion"
/lab_host="DH10B"

FEATURES
source
1. .34
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1440472"
/clone_lib="NCI CGAP PMS1"
/tissue_type="dorsal root ganglion"
/lab_host="DH10B"

BASE COUNT 5 a 10 c 17 g 2 t
ORIGIN
Query Match 36.7%; Score 11; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCGTGTGTC 11
|||||
Db 26 GGCGTGTGTC 16

/note="Organ: peripheral nervous system; Vector:
pCMV-SPORT4; Site 1: SalI; Site 2: NotI; Cloned
unidirectionally. Primer: Oligo dr. Average insert size
1.1 kb."
BASE COUNT 10 a 1 c 17 g 6 t
ORIGIN
Query Match 36.7%; Score 11; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTG 21
|||||
Db 28 CCATTTTGTG 18

RESULT 8
AI623585/c 34 bp mRNA linear EST 22-APR-1999
LOCUS ts37f06.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2230787 3'
DEFINITION similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15
PRECURSOR. ;, mRNA sequence.
ACCESSION AI623585
VERSION AI623585.1 GI:4648516
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
/db_xref="taxon:9606"
/clone="IMAGE:2230787"
/clone_lib="NCI CGAP Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"

REFERENCE
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL Tumor Gene Index
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40UP from Gibco
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GenCore version 5.1.6
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(without alignments)
2502.502 Million cell updates/sec

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3	29	96.7	30	6	A84596	A84596 Sequence 6
4	29	96.7	30	6	AR079893	AR079893 Sequence
5	29	96.7	30	6	AR063850	AR063850 Sequence
6	23	76.7	27	6	AX317989	AX317989 Sequence 2
7	22	73.3	26	6	A94988	A94988 Sequence 2
8	22	73.3	26	6	AR016055	AR016055 Sequence
9	22	73.3	26	6	AR028786	AR028786 Sequence
10	22	73.3	26	6	AR059216	AR059216 Sequence
11	22	73.3	26	6	AR075527	AR075527 Sequence
12	22	73.3	26	6	AR161925	AR161925 Sequence
13	22	73.3	26	6	AX022187	AX022187 Sequence
14	22	73.3	26	6	AX033377	AX033377 Sequence
15	22	73.3	26	6	AX468455	AX468455 Sequence
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18	22	73.3	26	6	E37046	E37046 Human telom
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AUTHORS
TITLE
JOURNAL
FEATURES

AR063832
Sequence 8 from patent US 5846723.
AR063832
AR063832.1 GI:5993140
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 30)
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 8 08-DEC-1998;
Location/Qualifiers

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PAT 29-SEP-1999

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ACCESSION  AX465471
VERSION     AX465471.1 GI:21899833
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ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Letsinger,R.L. and Garimella,V.
TITLE       Method of detection by enhancement of silver staining
JOURNAL     Patent: WO 0204681-A 2 17-JAN-2002;
NORTHWESTERN UNIVERSITY (US)
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ACCESSION  A84596
VERSION     A84596.1 GI:6733512
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SOURCE      unidentified
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REFERENCE   1 (bases 1 to 30)
AUTHORS     Atkinson,E.M. and Kealey,J.T.
TITLE       PURIFIED TELOMERASE
JOURNAL     Patent: WO 9845450-A 6 15-OCT-1998;
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ACCESSION  AR079893
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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vasserot,A.P.,
            Pruzan,R.A. and Kealey,J.T.
TITLE       Purified telomerase
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AUTHORS     Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE       Methods for detecting the RNA component of telomerase
JOURNAL     Patent: US 5846723-A 26 08-DEC-1998;
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ACCESSION  AX317989
VERSION     AX317989.1 GI:17900798
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REFERENCE Chen, X.Q. and Anker, P.
TITLE Cancer diagnosis method
JOURNAL Patent: WO 0190409-A 2 29-NOV-2001;
Chen, Xu Qi (US); Stroun, Maurice (CH); Anker, Philippe (CH)
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ACCESSION A94988
VERSION A94988.1 GI:6779168
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REFERENCE 1 (bases 1 to 26)
AUTHORS Emrich, T.D.
TITLE Method for detection of carcinoma of the urinary bladder within a
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PATENT: EP 0926245-A 2 30-JUN-1999;
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ACCESSION A016055
VERSION A016055.1 GI:3972332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
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REFERENCE Chen, X.Q. and Anker, P.
TITLE Cancer diagnosis method
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AUTHORS Emrich, T.D.
TITLE Method for detection of carcinoma of the urinary bladder within a
JOURNAL urine sample
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AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
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ACCESSION A028786
VERSION A028786.1 GI:5940759
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SOURCE Unknown.
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REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau, B., Feng, J., Andrews, W.H. and Adams, R.R.
TITLE Methods and reagents for regulating telomere length and telomerase
JOURNAL activity
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE Mammalian telomerase
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  Andrews,W.H., Villeponteau,B., Adams,R.R. and Peng,J.
  Methods and reagents for regulating telomere length and telomerase
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  Larsen,F. and Skaanseng,M.
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  TITLE
  JOURNAL
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  LARSEN FRANK (NO); SKAANSENG MARIANNE (NO)
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  Koprski,M.S. and Gocke,C.D.
  Method for detection of htr and htert telomerase-associated rna in
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GenCore version 5.1.6
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Sequence: 1 GCTCTAGATGAACGGTGAAGCGCAGG 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	73.3	26	9	US-10-044-692-312
2	22	73.3	26	9	US-10-044-692-312
3	22	73.3	26	10	US-09-057-351-23
4	13	43.3	25	9	US-10-098-263B-118949
5	13	43.3	26	9	US-09-952-522B-19
6	13	43.3	26	10	US-09-844-06A-3
7	13	43.3	46	10	US-09-780-566-11
8	12	40.0	23	9	US-09-969-373-1959
9	12	40.0	23	9	US-09-952-522B-17
10	12	40.0	23	9	US-09-952-522B-31
11	12	40.0	24	9	US-09-754-853A-676
12	12	40.0	24	9	US-09-940-185-3143
13	12	40.0	25	9	US-10-215-112-6862
14	12	40.0	25	9	US-10-215-112-8975
15	12	40.0	25	9	US-10-215-112-13825
16	12	40.0	25	9	US-10-098-263B-64498
17	12	40.0	26	9	US-10-011-366-16
18	12	40.0	34	9	US-09-430-029-11
19	11	36.7	17	9	US-09-930-423-1300

20	11	36.7	17	9	US-09-930-423-1688	Sequence 1688, Ap
21	11	36.7	17	9	US-09-930-423-1689	Sequence 1689, Ap
22	11	36.7	17	9	US-09-930-423-1690	Sequence 1690, Ap
23	11	36.7	17	10	US-09-866-108-2559	Sequence 2559, Ap
24	11	36.7	17	10	US-09-866-108-2560	Sequence 2560, Ap
25	11	36.7	17	10	US-09-866-108-2561	Sequence 2561, Ap
26	11	36.7	17	10	US-09-866-108-2562	Sequence 2562, Ap
27	11	36.7	17	10	US-09-866-108-2563	Sequence 2563, Ap
28	11	36.7	17	10	US-09-866-108-2564	Sequence 2564, Ap
29	11	36.7	17	10	US-09-866-108-2565	Sequence 2565, Ap
30	11	36.7	21	9	US-09-997-868-13	Sequence 13, Appl
31	11	36.7	22	10	US-09-785-873A-5	Sequence 5, Appl
32	11	36.7	23	9	US-09-952-522B-9	Sequence 2, Appl
33	11	36.7	24	9	US-10-245-813-2	Sequence 1005, Ap
34	11	36.7	24	9	US-09-940-185-1005	Sequence 11, Appl
35	11	36.7	24	10	US-09-757-041-11	Sequence 243, App
36	11	36.7	25	9	US-09-992-665-243	Sequence 10750, A
37	11	36.7	25	9	US-10-098-263B-10750	Sequence 22667, A
38	11	36.7	25	9	US-10-098-263B-22667	Sequence 33532, A
39	11	36.7	25	9	US-10-098-263B-33532	Sequence 44593, A
40	11	36.7	25	9	US-10-098-263B-44593	Sequence 44594, A
41	11	36.7	25	9	US-10-098-263B-44594	Sequence 104702, A
42	11	36.7	25	9	US-10-098-263B-104702	Sequence 117265, A
43	11	36.7	25	9	US-10-098-263B-117265	Sequence 5488, Ap
44	11	36.7	25	10	US-09-866-108-5488	Sequence 5489, Ap
45	11	36.7	25	10	US-09-866-108-5489	

ALIGNMENTS

RESULT 1
US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGGAG 22
|||||
Db 5 GCTCTAGAATGACGGTGGGAG 26

RESULT 2

US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 312:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 312:

US-10-044-539-312

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGGAG 22
|||||
Db 5 GCTCTAGAATGACGGTGGGAG 26

RESULT 3

US-09-057-351-23

Sequence 23, Application US/09057351

Patent No. US20010034439A1

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,351

FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match      73.3%; Score 22; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAG 22
   |||||
Db 5 GCTCTAGTAATGAACGGTGAAG 26

RESULT 4
US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match      43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGTAATGAACG 15
   |||||
Db 20 TCTAGTAATGAACG 8

RESULT 5
US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77UR11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer

US-09-952-522B-19
Query Match      43.3%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAA 13
   |||||
Db 1 GCTCTAGTAATGAA 13

RESULT 6
US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match      43.3%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAA 13
   |||||
Db 1 GCTCTAGTAATGAA 13

RESULT 7
US-09-780-566-11/c
; Sequence 11, Application US/09780566
; Patent No. US20020111289A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Herweking, Heiko
; TITLE OF INVENTION: CDK4 IS A TARGET OF C-MYC
; FILE REFERENCE: 01107.00092
; CURRENT APPLICATION NUMBER: US/09/780,566
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,930
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primers
US-09-780-566-11

Query Match      43.3%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 GGTGAAGCGGC 27
 Db 24 GGTGAAGCGGC 12

RESULT 8
 US-09-969-373-1959
 ; Sequence 1959, Application US/09969373
 ; Patent No. US20020133852A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Effertz, Roger J.
 ; APPLICANT: Hauge, Brian M.
 ; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
 ; FILE REFERENCE: 38-10(52679)A
 ; CURRENT APPLICATION NUMBER: US/09/969,373
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 09/754,853
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 09/760,427
 ; PRIOR FILING DATE: 2001-01-13
 ; PRIOR APPLICATION NUMBER: US 09/855,768
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 4593
 ; SEQ ID NO 1959
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-969-373-1959

Query Match 40.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Qy 9 ATGAACGGTGG 20
 Db 6 ATGAACGGTGG 17

RESULT 9
 US-09-952-522B-17
 ; Sequence 17, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benhaim, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; APPLICANT: Zhu, Min
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448.77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
 ; OTHER INFORMATION: forward primer
 US-09-952-522B-17

Query Match 40.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 GCTCTAGATGA 12
 Db 1 GCTCTAGATGA 12

RESULT 10
 US-09-952-522B-31
 ; Sequence 31, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benhaim, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; APPLICANT: Zhu, Min
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448.77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
 ; OTHER INFORMATION: forward primer
 US-09-952-522B-31

Query Match 40.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GCTCTAGATGA 12
 Db 1 GCTCTAGATGA 12

RESULT 11
 US-09-754-853A-676
 ; Sequence 676, Application US/09754853A
 ; Publication No. US20030005491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hauge, Brian M.
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Parsons, Jeremy D.
 ; APPLICANT: Wang, Ming Li
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
 ; FILE REFERENCE: 38-10(15810)B
 ; FILE REFERENCE: 38-10(15810)B
 ; CURRENT APPLICATION NUMBER: US/09/754,853A
 ; CURRENT FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 60/174,880
 ; PRIOR FILING DATE: 2000-01-07
 ; NUMBER OF SEQ ID NOS: 1119
 ; SEQ ID NO 676
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:

; OTHER INFORMATION: Clone ID: 318013_region_A3_187577_13_Reverse_Primer_Seq
US-09-754-853A-676

Query Match 40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGGG 20
DB 13 ATGAACGGTGGG 24
|||||

RESULT 12
US-09-940-185-3143/c
; Sequence 3143, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3143
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-3143
Query Match 40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACGGTGGAGGC 24
DB 16 ACGGTGGAGGC 5
|||||

RESULT 13
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-6862
Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
|||||

Db

15 GCTCTAGATGA 4

RESULT 14
US-10-215-112-8975
; Sequence 8975, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8975
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-8975
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Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGAAG 22
DB 5 GAACGGTGAAG 16
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RESULT 15
US-10-215-112-13825/c
; Sequence 13825, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13825
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-13825
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Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGAAG 22
DB 21 GAACGGTGAAG 10
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Search completed: June 23, 2003, 20:01:32
Job time : 242.076 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTCTAGATGAACCGTGAAGCGGCGAGG 30

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 68: /cgn2_6/ptodata/2/pna/US6024 COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6025 COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6026 COMB.seq.*
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- 73: /cgn2_6/ptodata/2/pna/US6029 COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6031 COMB.seq.*
- 76: /cgn2_6/ptodata/2/pna/US6032 COMB.seq.*
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- 78: /cgn2_6/ptodata/2/pna/US6034 COMB.seq.*
- 79: /cgn2_6/ptodata/2/pna/US6035 COMB.seq.*
- 80: /cgn2_6/ptodata/2/pna/US6036 COMB.seq.*
- 81: /cgn2_6/ptodata/2/pna/US6037 COMB.seq.*
- 82: /cgn2_6/ptodata/2/pna/US6038 COMB.seq.*
- 83: /cgn2_6/ptodata/2/pna/US6039 COMB.seq.*
- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	PCT-US97-23619-8
2	30	100.0	30	9	US-08-510-736-5
3	30	100.0	30	11	US-08-770-564A-8
4	30	100.0	30	21	US-09-540-119B-10
5	30	100.0	30	28	US-09-717-828A-5
6	30	100.0	30	28	US-09-717-828B-5
7	30	100.0	30	28	US-09-717-829A-5
8	30	100.0	30	34	US-09-903-461-2
9	23	76.7	27	1	PCT-US97-23619-26
10	22	73.3	25	16	US-09-250-336A-4
11	22	73.3	25	25	US-09-642-177-4
12	22	73.3	26	1	PCT-US96-14679-27
13	22	73.3	26	1	PCT-US99-03302-4
14	22	73.3	26	1	PCT-US99-07533-4
15	22	73.3	26	1	PCT-US99-07533-4
16	22	73.3	26	1	PCT-US99-07533-4
17	22	73.3	26	6	US-08-272-102-23
18	22	73.3	26	7	US-08-387-524-19
19	22	73.3	26	8	US-08-472-802A-24
20	22	73.3	26	8	US-08-472-802B-24
21	22	73.3	26	8	US-08-482-115A-23

US-08-770-564A-8
; Sequence 8, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-8

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
Db 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 4
US-09-540-119B-10
; Sequence 10, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-10

Query Match 100.0%; Score 30; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
Db 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 5
US-09-717-828A-5
; Sequence 5, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-5

Query Match 100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
Db 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 6
US-09-717-828B-5
; Sequence 5, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828B-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

RESULT 7
US-09-717-829A-5
; Sequence 5, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1 edited
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

RESULT 8
US-09-903-461-2
; Sequence 2, Application US/09903461
; GENERAL INFORMATION:
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Garimella, Viswanadham
; TITLE OF INVENTION: Method of Detection by Enhancement of Silver Staining
; FILE REFERENCE: 09-1086-A
; CURRENT APPLICATION NUMBER: US/09/903,461
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/217,782
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 98
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-09-903-461-2

Query Match      100.0%; Score 30; DB 34; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

RESULT 9
PCT-US97-23619-26
; Sequence 26, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..27
; OTHER INFORMATION: /note= "hTR reverse primer"
PCT-US97-23619-26

Query Match      76.7%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGG 23
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Db 5 GCTCTAGATGAACGGTGAAG 27
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RESULT 10
US-09-250-336A-4
; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 73.3%; Score 22; DB 16; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
|||||

Db 4 GCTCTAGATGAACGGTGAAG 25
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RESULT 11
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; TITLE OF INVENTION: 10460-4U1 (210460.0019)
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 73.3%; Score 22; DB 25; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

Db 4 GCTCTAGATGAACGGTGAAG 25
|||||

RESULT 12
PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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Db 5 GCTCTAGATGAACGGTGAAG 26
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RESULT 13
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 1316.89 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0
Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	30	10	US-10-330-872-5
2	30	100.0	30	10	US-10-330-872A-5
3	23	76.7	23	1	PCT-US03-04088-520
4	22	73.3	23	1	PCT-US03-04088-529
5	22	73.3	26	6	US-09-721-456-598
6	22	73.3	26	9	US-10-325-810-598
7	22	73.3	26	9	US-10-359-935-23
8	21	70.0	21	1	PCT-US03-04088-587
9	21	70.0	23	1	PCT-US03-04088-521
10	20	66.7	21	1	PCT-US03-04088-592
11	19	63.3	19	1	PCT-US03-04088-14
12	19	63.3	19	1	PCT-US03-04088-257
13	19	63.3	19	1	PCT-US03-04088-278
14	19	63.3	21	1	PCT-US03-04088-538
15	19	63.3	21	1	PCT-US03-04088-539
16	19	63.3	21	1	PCT-US03-04088-542
17	19	63.3	21	1	PCT-US03-04088-543
18	19	63.3	21	1	PCT-US03-04088-546
19	19	63.3	21	1	PCT-US03-04088-547
20	19	63.3	21	1	PCT-US03-04088-550

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c 22	19	63.3	21	1	PCT-US03-04088-554	Sequence 554, App
c 23	19	63.3	21	1	PCT-US03-04088-555	Sequence 555, App
24	19	63.3	21	1	PCT-US03-04088-558	Sequence 558, App
25	19	63.3	21	1	PCT-US03-04088-559	Sequence 559, App
c 26	14	46.7	23	9	US-10-310-188-36216	Sequence 36216, A
27	14	46.7	24	8	US-10-442-506-39	Sequence 39, Appl
28	14	46.7	25	12	US-60-427-808-952738	Sequence 952738, A
29	14	46.7	25	13	US-60-469-545-13722	Sequence 13722, A
c 30	14	46.7	25	13	US-60-469-545-222991	Sequence 222991, A
31	13	43.3	18	6	US-09-721-456-543	Sequence 543, App
32	13	43.3	18	9	US-10-325-810-543	Sequence 543, App
c 33	13	43.3	25	6	US-09-660-222-3845	Sequence 3845, App
c 34	13	43.3	25	6	US-09-660-222-3846	Sequence 3846, App
c 35	13	43.3	25	6	US-09-660-222-3854	Sequence 3854, App
c 36	13	43.3	25	9	US-10-098-263B-118949	Sequence 118949, A
c 37	13	43.3	25	9	US-10-355-577-90268	Sequence 90268, A
c 38	13	43.3	25	9	US-10-355-577-173196	Sequence 173196, A
c 39	13	43.3	25	9	US-10-355-577-231533	Sequence 231533, A
c 40	13	43.3	25	9	US-10-355-577-579523	Sequence 579523, A
c 41	13	43.3	25	12	US-60-427-808-738286	Sequence 738286, A
c 42	13	43.3	25	12	US-60-427-808-843246	Sequence 843246, A
c 43	13	43.3	25	12	US-60-427-836-69383	Sequence 69383, A
c 44	13	43.3	25	12	US-60-427-836-267834	Sequence 267834, A
c 45	12	40.0	18	9	US-10-310-188-60169	Sequence 60169, A

ALIGNMENTS

RESULT 1
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30
Db 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30

RESULT 2
US-10-330-872A-5
; Sequence 5, Application US/10330872A

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Weinrich, Scott
APPLICANT: Atkinson III, Edward
APPLICANT: Lichtsteiner, Serge
APPLICANT: Vasserot, Alain
APPLICANT: Pruzan, Ronald
TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and Inhibitors
FILE REFERENCE: 011/006C
CURRENT APPLICATION NUMBER: US/10/330,872A
CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: 08/510,736
PRIOR FILING DATE: 1995-08-04
PRIOR APPLICATION NUMBER: 08/933,377
PRIOR FILING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: 09/420,056
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/717,828
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGAAGCGGCAGG 30

RESULT 3
PCT-US03-04088-520/c
Sequence 520, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 520
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region

OTHER INFORMATION: region
PCT-US03-04088-520
Query Match 76.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGAAGG 23
DB 23 GCTCTAGATGAACGGTGAAGG 1
RESULT 4
PCT-US03-04088-529/c
Sequence 529, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 529
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGAAGCGGCAGG 30
DB 23 ATGAACGGTGAAGCGGCAGG 2

RESULT 5
US-09-721-456-598
Sequence 598, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598

Query Match 73.3%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB 5 GCTCTAGATGAACGGTGAAG 26
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RESULT 6
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:

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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Ausubelus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 7

US-10-359-935-23

; Sequence 23, Application US/10359935

; GENERAL INFORMATION:

; APPLICANT: Villeponteau, Bryant

; Peng, Junli

; Funk, Walter

; Andrews, William H.

; TITLE OF INVENTION: Mammalian Telomerase

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/359,935

; FILING DATE: 07-Feb-2003

; CLASSIFICATION DATA:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/057,351

; FILING DATE: 08-APR-1994

; APPLICATION NUMBER: US 08/272,102

; FILING DATE: 07-JUL-1994

; APPLICATION NUMBER: US 08/330,123

; FILING DATE: 27-OCT-1994

; APPLICATION NUMBER: US 08/472,802

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-000821US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-359-935-23

Query Match 73.3%; Score 22; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0089;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGAAG 22

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Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 8

PCT-US03-04088-587/c

; Sequence 587, Application PC/TUS0304088

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; Applicant: McSwiggen, James

; Applicant: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

; ;

; FILE REFERENCE: 02-708-A (400/080)

; CURRENT APPLICATION NUMBER: PCT/US03/04088

; CURRENT FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/396,600

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 587

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

; OTHER INFORMATION: region

PCT-US03-04088-587

Query Match 70.0%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.034;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGAACGGCGCAG 29

|||||

Db 21 ATGAACGGTGAACGGCGCAG 1

RESULT 9

PCT-US03-04088-521/c

; Sequence 521, Application PC/TUS0304088

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; Applicant: McSwiggen, James

; Applicant: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

; ;

; FILE REFERENCE: 02-708-A (400/080)

; CURRENT APPLICATION NUMBER: PCT/US03/04088

; CURRENT FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/396,600

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 521

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-521

Query Match 70.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.034; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 GCTCTAGATGAACGGTGAA 21
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Db 21 GCTCTAGATGAACGGTGAA 1

RESULT 10
PCT-US03-04088-592
Sequence 592, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent in version 3.2
SEQ ID NO 592
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
PCT-US03-04088-592

Query Match 66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 0.13;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 11 GAACGGTGAAGCGGCAGG 30
|||||
Db 1 GAACGGTGAAGCGGCAGG 20

RESULT 11
PCT-US03-04088-14/c
Sequence 14, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088

CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent in version 3.2
SEQ ID NO 14
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-14

Query Match 63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 9 ATGAACGGTGAAGCGGC 27
|||||
Db 19 ATGAACGGTGAAGCGGC 1

RESULT 12
PCT-US03-04088-257/c
Sequence 257, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent in version 3.2
SEQ ID NO 257
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

```
; OTHER INFORMATION: region
PCT-US03-04088-257

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 GAACGGTGAAGCGGCGAG 29
Db 19 GAACGGTGAAGCGGCGAG 1

RESULT 13
PCT-US03-04088-278
; Sequence 278, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 0.49;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 9 ATGAACGGTGAAGCGGCGC 27
Db 1 AUGAACGGUGGAAGCGGC 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600

; OTHER INFORMATION: region
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 GAACGGTGAAGCGGCGAG 29
Db 19 GAACGGTGAAGCGGCGAG 1

RESULT 15
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; OTHER INFORMATION: thymidine
PCT-US03-04088-538

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TCTAGAATGAACGGTGGA 21
Db 19 TCTAGAATGAACGGTGGA 1

RESULT 15
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; OTHER INFORMATION: thymidine
PCT-US03-04088-538
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; OTHER INFORMATION: Description of Artificial Sequence:  siNA sense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

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Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGATGAACGGTGG 19
         |||||
Db      19 GCTCTAGATGAACGGTGG 1

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Job time : 1317.89 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTTAGAATGAACGGTGAAGCGGCAGG 30

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
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17: gb_gss:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	37	9	AI358100 qv96c06.x
C 2	11	36.7	37	9	AA388365 vc94b10.r
C 3	11	36.7	38	9	AU256784 AU256784
C 4	11	36.7	40	12	BF234348 602026283
C 5	11	36.7	41	17	BH851717 SALK 0734
C 6	11	36.7	48	17	AZ606694 1M0428D15

C 7	11	36.7	50	9	AUI04491	AUI04491
C 8	11	36.7	50	9	AUI04493	AUI04493
C 9	10	33.3	19	17	AZ471573	IM0286G13
C 10	10	33.3	28	17	TA116E03P	AL462526 T. brucei
C 11	10	33.3	29	17	TA264G10Q	AL487013 T. brucei
C 12	10	33.3	31	9	AA912698	ol30e02.s
C 13	10	33.3	31	17	TA106A06P	AU459090 T. brucei
C 14	10	33.3	34	10	AV964763	AV964763
C 15	10	33.3	34	14	T74961	T74961 yc85b03.r1
C 16	10	33.3	43	17	BH811442	SALK 0586
C 17	10	33.3	46	9	AA681423	AA681423 vr41f08.s
C 18	10	33.3	46	13	BI822830	BI822830 603040148
C 19	10	33.3	49	17	AZ971265	AZ971265 2M0244N12
C 20	10	33.3	49	17	BH791685	BH791685 SALK 0608
C 21	10	33.3	50	9	AUI03954	AUI03954 AUI03954
C 22	10	33.3	50	9	AUI04288	AUI04288 AUI04288
C 23	10	33.3	50	9	AUI04289	AUI04289 AUI04289
C 24	10	33.3	50	9	AUI04290	AUI04290 AUI04290
C 25	10	33.3	50	9	AUI04291	AUI04291 AUI04291
C 26	10	33.3	50	9	AUI04292	AUI04292 AUI04292
C 27	10	33.3	50	9	AUI04294	AUI04294 AUI04294
C 28	10	33.3	50	9	AUI04295	AUI04295 AUI04295
C 29	10	33.3	50	9	AUI04299	AUI04299 AUI04299
C 30	10	33.3	50	9	AUI04305	AUI04305 AUI04305
C 31	10	33.3	50	9	AUI04306	AUI04306 AUI04306
C 32	10	33.3	50	9	AUI07444	AUI07444 AUI07444
C 33	10	33.3	50	9	AUI07670	AUI07670 AUI07670
C 34	10	33.3	50	9	AUI07671	AUI07671 AUI07671
C 35	10	33.3	50	9	AUI07673	AUI07673 AUI07673
C 36	10	33.3	50	9	AUI07674	AUI07674 AUI07674
C 37	10	33.3	50	9	AUI07679	AUI07679 AUI07679
C 38	10	33.3	50	9	AUI07681	AUI07681 AUI07681
C 39	10	33.3	50	9	AUI07682	AUI07682 AUI07682
C 40	10	33.3	50	9	AUI07683	AUI07683 AUI07683
C 41	10	33.3	50	9	AUI07930	AUI07930 AUI07930
C 42	10	33.3	50	9	AUI07932	AUI07932 AUI07932
C 43	10	33.3	50	17	AZ920773	AZ920773 1006022E0
C 44	9	30.0	22	9	AU259636	AU259636
C 45	9	30.0	24	17	AZ662500	AZ662500 1M0541G07

ALIGNMENTS

RESULT 1
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LOCUS qv96c06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:1989418 3'
DEFINITION similar to SW:UIC6_HCMVA F16836 HYPOTHETICAL PROTEIN UL126. ; mRNA
sequence.
ACCESSION AI358100
VERSION AI358100 GI:4109721
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmer-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 37
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/db_xref="taxon:9606"
/clone="IMAGE:1989418"
/clone_lib="NCI CGAP Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

BASE COUNT 4 a 18 c 4 g 11 t
ORIGIN

Query Match 40.0%; Score 12; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e+04; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGTGGAAGCGG 26
Db 31 GGTGGAAGCGG 20

RESULT 2
AA388365/c
LOCUS
DEFINITION
VC94B10.r1 Barstead MPLRBI Mus musculus cDNA clone IMAGE:790651 5'
Similar to TR:G624778 G624778 E25. ;, mRNA sequence.
AA388365
ACCESSION
AA388365.1 GI:2041335
VERSION
AA388365.1 GI:2041335
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Streptoc, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:475059
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 37
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:790651"
/clone_lib="Barstead MPLRBI"
/sex="mixed"
/tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"

BASE COUNT 8 a 11 c 7 g 11 t
ORIGIN

Query Match 36.7%; Score 11; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.9e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AACGTTGGAG 22
Db 31 AACGTTGGAG 21

RESULT 3
AU256784/c
LOCUS
DEFINITION
AU256784 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0008969 3', mRNA sequence.
AU256784
ACCESSION
AU256784.1 GI:20320773
VERSION
AU256784.1 GI:20320773
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 38)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kato@obs.aist-nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
1. 38
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0008969"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"
/note="Vector: pGEM-T-easy"

BASE COUNT 2 a 22 c 3 g 11 t
ORIGIN

Query Match 36.7%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.9e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
Db 17 GGAAGCGGCA 7

RESULT 4
BF234348/c
LOCUS
DEFINITION
602026283F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4161429 5',
mRNA sequence.
BF234348
ACCESSION
BF234348.1 GI:11145738
VERSION
BF234348.1 GI:11145738
KEYWORDS
EST.
SOURCE
house mouse.

BASE COUNT 2 a 22 c 3 g 11 t
ORIGIN

Query Match 36.7%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.9e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
Db 17 GGAAGCGGCA 7


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ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          NIH-MGC http://mgc.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs@mail.nih.gov
               Tissue Procurement: Jeffrey E. Green, M.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM9442 row: f column: 22
               High quality sequence stop: 40.
               Location/Qualifiers
                 1..40
                   /organism="Mus musculus"
                   /strain="FVB/N"
                   /db_xref="taxon:10090"
                   /clone="IMAGE:4161429"
                   /clone_lib="NCI_CGAP_Li9"
                   /lab_host="DH10B (T1 phage-resistant)"
                   /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                   Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
                   Average insert size 1.9 kb. Constructed by Life
                   Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT    3 a 12 c 13 g 12 t
ORIGIN
Query Match      36.7%; Score 11; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGAAGCGCGCA 28
        |||||
        29 GGAAGCGCGCA 19

RESULT 5
BH851717/c
LOCUS      BH851717
DEFINITION BH851717 41 bp DNA linear GSS 13-JUN-2002
            SALK_073411.49.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_073411.49.55.x, DNA
            sequence.
ACCESSION  BH851717
VERSION    BH851717.1 GI:21422588
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana
            thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 41)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL    Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.

Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          NIH-MGC http://mgc.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs@mail.nih.gov
               Tissue Procurement: Jeffrey E. Green, M.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM9442 row: f column: 22
               High quality sequence stop: 40.
               Location/Qualifiers
                 1..40
                   /organism="Mus musculus"
                   /strain="FVB/N"
                   /db_xref="taxon:10090"
                   /clone="IMAGE:4161429"
                   /clone_lib="NCI_CGAP_Li9"
                   /lab_host="DH10B (T1 phage-resistant)"
                   /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                   Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
                   Average insert size 1.9 kb. Constructed by Life
                   Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT    3 a 12 c 13 g 12 t
ORIGIN
Query Match      36.7%; Score 11; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGAAGCGCGCA 28
        |||||
        29 GGAAGCGCGCA 19

RESULT 6
AZ606694
LOCUS      AZ606694
DEFINITION 1M0428D15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0428D15 R, DNA sequence.
ACCESSION  AZ606694
VERSION    AZ606694.1 GI:11728884
KEYWORDS   GSS.
SOURCE     house mouse.
            Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 48)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunne@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0428 row: D column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 48.
            Location/Qualifiers
              1..48
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0428D15"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA

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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 13 c 15 g 10 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 ATGACGGTGG 19
 Db 38 ATGACGGTGG 48
 |||||

RESULT 7
 AUI04491/c
 LOCUS
 DEFINITION AUI04491 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP22239, mRNA sequence.

ACCESSION AUI04491
 VERSION AUI04491.1 GI:13554012
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

TITLE
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1. .50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="HEP22239"

/clone_lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumurate treated U937 cells"
 3 a 26 c 13 g 8 t

BASE COUNT 3 a 26 c 13 g 8 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
 Db 28 GGAAGCGGCA 18
 |||||

RESULT 8

AUI04493/c
 LOCUS
 DEFINITION AUI04493 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ADKA03063, mRNA sequence.

ACCESSION AUI04493
 VERSION AUI04493
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

TITLE
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1. .50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="ADKA03063"

/clone_lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumurate treated U937 cells"
 4 a 26 c 13 g 7 t

BASE COUNT 4 a 26 c 13 g 7 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 4.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
 Db 33 GGAAGCGGCA 23
 |||||

RESULT 9

AZ471573/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

QY

Db

|||||

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4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
    source
        1. .28
            /organism="Trypanosoma brucei"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="116e03"

BASE COUNT      7 a  5 c  8 g  8 t
ORIGIN

Query Match      33.3%; Score 10; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      7 GAATGAACGG 16
        |||||
        2 GAATGAACGG 11

RESULT 11
TA264G10Q
LOCUS
DEFINITION      TA264G10Q      29 bp      DNA      linear      GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 264g10, reverse sequence,
genomic survey sequence.
ACCESSION      AL487013
VERSION      AL487013.1      GI:11850630
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei.
ORGANISM      Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Meiville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
    source
        1. .29
            /organism="Trypanosoma brucei"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="264g10"

BASE COUNT      11 a  5 c  11 g  2 t
ORIGIN

Query Match      33.3%; Score 10; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      6 AGAATGAACG 15

```

```

Db
|||||
7 AGAATGAACG 16

RESULT 12
AA912698
LOCUS
DEFINITION
O130e02.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1524986 3' similar to TR:O14564 O14564 HYPOTHETICAL 67.1 KD
PROTEIN. 1, mRNA sequence.
ACCESSION
AA912698
VERSION
AA912698.1 GI:3052090
KEYWORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 31)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 378 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1524986"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
viro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 8 a 7 c 12 g 4 t
ORIGIN
source
Query Match 33.3%; Score 10; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
21 AGCGCGCAGG 30
|||||
14 AGCGCGCAGG 23

RESULT 13
TA106A06P
LOCUS
DEFINITION
TA106A06P 31 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 106a06, forward sequence,
genomic survey sequence.
ACCESSION
AL459090
VERSION
AL459090.1 GI:11830967
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 31)

AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T\_brucei/.
Location/Qualifiers
1..31
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="106a06"
BASE COUNT 8 a 11 c 7 g 5 t
ORIGIN
source
Query Match 33.3%; Score 10; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
11 GAACGGTGGG 20
|||||
13 GAACGGTGGG 22

RESULT 14
AV964763/c
LOCUS
DEFINITION
AV964763 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad15006 5', mRNA sequence.
ACCESSION
AV964763
VERSION
AV964763.1 GI:19454459
KEYWORDS
EST.
SOURCE
Ciona intestinalis.
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in Ciona intestinalis
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="ciad15006"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/notes="Vector: pBluescript SK"
BASE COUNT 12 a 5 c 8 g 9 t
ORIGIN
source

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Db 11 TGAAGGCGG 20

Search completed: June 23, 2003, 10:10:24

Job time : 1548.89 secs

Query Match 33.3%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAAT 10
 |||||
 Db 16 GCTCTAGAAAT 7

RESULT 15

T74961 34 bp mRNA linear EST 07-MAR-1995

LOCUS YC85b03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone

DEFINITION IMAGE:22801 5' similar to SP:A27671 A27671 SPECTRIN ALPHA CHAIN, NONERYTHROID - RAT ;, mRNA sequence.

ACCESSION T74961

VERSION T74961.1 GI:691636

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 34)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1872

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 1872 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1..34

/organism="Homo sapiens"

/db_xref="GDB:395148"

/db_xref="taxon:9606"

/clone="IMAGE:22801"

/clone_lib="Soares infant brain 1N1B"

/sex="Female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',

1 - oligo(dT) primer [5',

ACTGAGAGATTCCGCCGCCGAGGAATTTTATTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 7 a 6 c 13 g 8 t

Query Match 33.3%; Score 10; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAAGGCGG 26
 |||||

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30
Sequence: 1 GCTCTAGTAATGAACGGTGGAGCGGCGAGG 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A-COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B-COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS-COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	US-08-770-565-8
2	29	96.7	30	2	US-08-833-377-6
3	23	76.7	27	2	US-08-770-565-26
4	22	73.3	26	1	US-08-330-123A-23
5	22	73.3	26	1	US-08-482-115B-23
6	22	73.3	26	2	US-08-660-678A-23
7	22	73.3	26	2	US-08-710-249-26
8	22	73.3	26	2	US-08-485-778-19
9	22	73.3	26	2	US-08-472-802C-24
10	22	73.3	26	3	US-08-520-550A-19
11	22	73.3	26	3	US-08-998-443-23
12	22	73.3	26	4	US-08-974-549A-598
13	22	73.3	26	4	US-09-060-523-23
14	22	73.3	26	4	US-09-220-157A-26
15	22	73.3	26	4	US-09-286-959B-4
16	22	73.3	26	4	US-09-580-517-23
17	19	63.3	19	2	US-08-770-565-9
18	16.8	56.0	27	3	US-08-630-172-24
19	16.8	56.0	27	4	US-09-375-419-24
20	16.4	54.7	18	4	US-08-974-549A-543
21	15.8	52.7	30	4	US-08-846-247-13
22	15.6	52.0	50	2	US-08-448-418-31
23	15.4	51.3	31	4	US-09-513-838-3
24	15.4	51.3	42	1	US-08-439-813-2
25	15.4	51.3	42	5	PT-US96-05291A-2
26	15	50.0	15	2	US-08-770-565-10
27	15	50.0	25	1	US-08-629-939-8

28	15	50.0	25	1	US-08-759-873-8	Sequence 8, Appli
29	14.6	48.7	40	1	US-08-411-795B-255	Sequence 255, App
30	14.6	48.7	40	1	US-08-469-319A-255	Sequence 255, App
31	14.6	48.7	40	4	US-08-764-114-255	Sequence 255, App
32	14.6	48.7	40	4	US-08-469-419-255	Sequence 255, App
33	14.6	48.7	41	1	US-08-411-795B-234	Sequence 234, App
34	14.6	48.7	41	1	US-08-469-319A-234	Sequence 234, App
35	14.6	48.7	41	4	US-08-764-114-234	Sequence 234, App
36	14.6	48.7	41	4	US-08-469-419-234	Sequence 234, App
37	14.6	48.7	45	1	US-08-411-795B-409	Sequence 409, App
38	14.6	48.7	45	1	US-08-469-319A-409	Sequence 409, App
39	14.6	48.7	45	4	US-08-764-114-409	Sequence 409, App
40	14.6	48.7	45	4	US-08-469-419-409	Sequence 409, App
41	14.4	48.0	37	1	US-08-591-492-17	Sequence 17, Appli
42	14.2	47.3	48	2	US-08-729-955A-9	Sequence 9, Appli
43	14.2	47.3	49	4	US-09-538-709-931	Sequence 931, App
44	14	46.7	28	4	US-09-033-333-18	Sequence 18, Appl
45	14	46.7	28	4	US-09-033-428-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-8
; Sequence 8, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-8

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred.No. 4.3e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
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US-08-833-377-6
; Sequence 6, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod base= OTHER
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"
; FEATURE:
; NAME/KEY:
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 14"
US-08-833-377-6
Query Match 96.7%; Score 29; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTAGATGAACGGTGGAGCGGCAGG 30
Db 2 CTCTAGATGAACGGTGGAGCGGCAGG 30
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RESULT 3
US-08-770-565-26
; Sequence 26, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-26
Query Match 76.7%; Score 23; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAGG 23
Db 5 GCTCTAGATGAACGGTGGAGG 27
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RESULT 4
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-2400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22
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Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 5
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villegontean, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22
|||||
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 6
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Villegontean, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22

Db 5 GCTCTAGATGACGGTGAAG 26
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RESULT 7
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26
Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATGACGGTGAAG 22
Db 5 GCTCTAGATGACGGTGAAG 26
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RESULT 8
US-08-485-778-19
; Sequence 19, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-778-19
Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATGACGGTGAAG 22
Db 5 GCTCTAGATGACGGTGAAG 26
|||||
RESULT 9
US-08-472-802C-24
; Sequence 24, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 10
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-19
Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26
RESULT 11
US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 12
US-08-974-549A-598
; Sequence 598, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION NUMBER: WO PCT/US97/17895

FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 13
US-09-060-523-23
; Sequence 23, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
NAME: Strella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 14

US-09-220-157A-26
; Sequence 26, Application US/09220157A
; Patent No. 6300110

; GENERAL INFORMATION:

; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220.157A
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/710.249

; FILING DATE: 13-SEP-1996

; APPLICATION NUMBER: US 08/583,808

; FILING DATE: 05-JAN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/003,492

; FILING DATE: 08-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-001220US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-09-220-157A-26

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 15

US-09-286-959B-4

; Sequence 4, Application US/09286959B

; Patent No. 6300131

; GENERAL INFORMATION:

; APPLICANT: Johns Hopkins University

; APPLICANT: Greider, Carol W.

; APPLICANT: Le, Siyuan

; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS

; FILE REFERENCE: 07265/157001

; CURRENT APPLICATION NUMBER: US/09/286.959B

; CURRENT FILING DATE: 1999-04-06

; PRIOR APPLICATION NUMBER: 60/080,783

; PRIOR FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-286-959B-4

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

Search completed: June 25, 2003, 00:24:39
Job time : 46.5378 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTTAGAATGACGGTGAAGCGGCAGG 30

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Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	22	73.3	26	9	US-10-044-539-312
3	22	73.3	26	10	US-09-057-351-23
4	15.8	52.7	30	9	US-09-852-416-31
5	15.8	52.7	30	9	US-10-096-789-13
6	15.8	52.7	30	9	US-10-096-790-10
7	15.8	52.7	30	10	US-09-859-854-31
8	15.4	51.3	31	9	US-10-139-483-3
9	14.6	48.7	40	9	US-10-090-182A-255
10	14.6	48.7	41	9	US-10-090-182A-234
11	14.6	48.7	45	9	US-10-090-182A-409
12	14.2	47.3	25	9	US-10-098-263B-51583
13	14	46.7	25	9	US-10-098-263B-81514
14	14	46.7	25	9	US-10-098-263B-105334
15	14	46.7	28	9	US-09-898-883-19
16	14	46.7	28	9	US-10-045-116-16
17	14	46.7	28	9	US-10-222-479-18
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19	14	46.7	28	10	US-09-875-228-25

Sequence 21, Appl
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Sequence 67, Appl
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Sequence 7103, Appl
Sequence 11, Appl
Sequence 4633, Appl
Sequence 4634, Appl
Sequence 31404, A
Sequence 72147, A
Sequence 25, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 235, Appl
Sequence 50, Appl
Sequence 8975, Appl
Sequence 13825, A
Sequence 27359, A
Sequence 27360, A
Sequence 93148, A
Sequence 6, Appl
Sequence 17930, A
Sequence 19, Appl
Sequence 77, Appl

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US-10-081-806-67
US-09-940-244-56
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US-10-098-263B-31404
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US-10-012-013-25
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US-09-748-451-13
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US-10-086-156-50
US-10-215-112-8975
US-10-215-112-13825
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US-10-098-263B-27360
US-10-098-263B-93148
US-09-850-964-6
US-10-098-263B-17930
US-09-952-522B-19
US-10-273-541-77

ALIGNMENTS

RESULT 1

US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

us-08-770-564a-8.rnpb

Fri Jun 27 07:43:12 2003

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; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGGAAG 22
Db 5 GCTCTAGATGAACGGTGGGAAG 26

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US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGGAAG 22
Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match      73.3%; Score 22; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGGAG 22
    |||||
Db 5 GCTCTAGAATGAACGGTGGAG 26

RESULT 4
US-09-852-416-31
; Sequence 31,, Application US/09852416
; Publication No. US20030040084A1
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Ashley, Gary
; APPLICANT: Fu, Hong
; APPLICANT: Kao, Camilla M.
; APPLICANT: McDaniel, Robert
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER AS SCAFFOLD
; FILE REFERENCE: 30062-20005.02
; CURRENT APPLICATION NUMBER: US/09/852,416
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/859,854
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/US98/08792
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/076,919
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/846,247
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: 08/486,645
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/238,811
; PRIOR FILING DATE: 1994-05-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Module rapDH/ER/KR1 (reverse) Primer pairs used
; OTHER INFORMATION: for PCR amplification of rapamycin PKS cassettes.
US-09-852-416-31

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTAGAATGAACGGTGGAGCGGCAG 29
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Db 4 TCTAGAATCAACGGTGAAGCAGCCG 30

RESULT 5
US-10-096-789-13
; Sequence 13, Application US/10096789
; Publication No. US2003007760A1
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Ashley, Gary
; APPLICANT: Fu, Hong
; APPLICANT: McDaniel, Robert
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER
; AS SCAFFOLD
US-10-096-789-13

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTAGAATGAACGGTGGAGCGGCAG 29
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Db 4 TCTAGAATCAACGGTGAAGCAGCCG 30

RESULT 6
US-10-096-790-10
; Sequence 10, Application US/10096790
; Publication No. US2003007770A1
; GENERAL INFORMATION:
; APPLICANT: Kossan Biosciences, Inc.
; APPLICANT: Khosla, Chaitan
; APPLICANT: Kao, Camilla
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER AS SCAFFOLD
; FILE REFERENCE: 30062-20005.03
; CURRENT APPLICATION NUMBER: US/10/096,790
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/076,919
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/003,338
; PRIOR FILING DATE: 1995-07-06
; PRIOR APPLICATION NUMBER: US 08/846,247
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: US 08/486,645
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/238,811
; PRIOR FILING DATE: 1994-05-06

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; PRIOR APPLICATION NUMBER: US/08/164,301
; PRIOR FILING DATE: 1993-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer rapDH/ER/KR1 (right half) (reverse)
US-10-096-790-10

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTAGAAATGACCGGTGAAGCGGCAG 29
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Db 4 TCTAGAAATCACCAGGTAGAAGCAGCCCG 30

RESULT 7
US-09-859-854-31
; Sequence 31, Application US/09859854
; Patent No. US20020068332A1
; GENERAL INFORMATION:
; APPLICANT: PKhosla, Chaitan
; APPLICANT: Ashley, Gary
; APPLICANT: Fu, Hong
; APPLICANT: Kao, Camilla M.
; APPLICANT: McDaniel, Robert
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; FILE REFERENCE: 30062-20005.02
; CURRENT APPLICATION NUMBER: US/09/859,854
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/US98/08792
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/076,919
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/846,247
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: 08/486,645
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/238,811
; PRIOR FILING DATE: 1994-05-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Module rapDH/ER/KR1 (reverse) Primer pairs used
; OTHER INFORMATION: for PCR amplification of rapamycin PKS cassettes.
US-09-859-854-31

Query Match      52.7%; Score 15.8; DB 10; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTAGAAATGACCGGTGAAGCGGCAG 29
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Db 4 TCTAGAAATCACCAGGTAGAAGCAGCCCG 30

RESULT 8
US-10-139-483-3
; Sequence 3, Application US/10139483
; Publication No. US20030055266A1
; GENERAL INFORMATION:
; APPLICANT: Beeley, Nigel R
; APPLICANT: Behan, Dominic P

; APPLICANT: Chalmers, Derek T
; APPLICANT: Menzaghi, Frederique
; APPLICANT: Strah-Pleyret, Sonja
; TITLE OF INVENTION: Small Molecule Modulators Of G Protein-Coupled Receptor
; TITLE OF INVENTION: Six
; FILE REFERENCE: AREN0058
; CURRENT APPLICATION NUMBER: US/10/139,483
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/513,838
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/364,425
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-139-483-3

Query Match      51.3%; Score 15.4; DB 9; Length 31;
Best Local Similarity 76.0%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CTCTAGAAATGAACGGTGAAGCGCG 26
    |||||
Db 4 CTCTAGAAATGACGGGTGCAAAATCCG 28

RESULT 9
US-10-090-182A-255
; Sequence 255, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kumanan
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides
; NUMBER OF SEQUENCES: 415
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/090,182A
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/764,114
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION NUMBER: PCT/US93/11197
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/411,795
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;; FILING DATE: 04-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C2713/12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (736)737-6257
;; INFORMATION FOR SEQ ID NO: 255:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (synthetic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 255:
US-10-090-182A-255

Query Match 48.7%; Score 14.6; DB 9; Length 40;
Best Local Similarity 81.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGTAAGTGAACGGTGGAA 21
||||| ||||| ||||| ||||| |||||
Db 12 GCTCTATATGATCGATGAAA 32

RESULT 10
US-10-090-182A-234
; Sequence 234, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olines, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides
; NUMBER OF SEQUENCES: 415
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
; Corporate Patent Dept. Mail Zone 04E
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/090,182A
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/764,114
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION NUMBER: PCT/US93/11197
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/411,795
; FILING DATE: 04-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305

;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C2713/12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (736)737-6257
;; INFORMATION FOR SEQ ID NO: 234:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (synthetic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 234:
US-10-090-182A-234

Query Match 48.7%; Score 14.6; DB 9; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGTAAGTGAACGGTGGAA 21
||||| ||||| ||||| ||||| |||||
Db 12 GCTCTATATGATCGATGAAA 32

RESULT 11
US-10-090-182A-409/c
; Sequence 409, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olines, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides
; NUMBER OF SEQUENCES: 415
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
; Corporate Patent Dept. Mail Zone 04E
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/090,182A
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/764,114
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION NUMBER: PCT/US93/11197
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/411,795
; FILING DATE: 04-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305

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; REFERENCE/DOCKET NUMBER: C2713/12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (636)737-6257
; TELEFAX: (736)737-6257
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 409:
US-10-090-182A-409

Query Match 48.7%; Score 14.6; DB 9; Length 45;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAA 21
Db 38 GCTCTATAATGATCGATGAA 18

RESULT 12
US-10-098-263B-51583
; Sequence 51583, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-51583

Query Match 47.3%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCTAGATGAACGGTGG 20
Db 7 CTCTAGAGTCAACGCTGA 25

RESULT 13
US-10-098-263B-81514/c
; Sequence 81514, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81514
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81514

Query Match 46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CTCTAGATGAACGGTGGAGG 23
Db 24 CTCTAGAAGGTACGGGTAGG 3

RESULT 14
US-10-098-263B-105334/c
; Sequence 105334, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105334

Query Match 46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTAGAATGAACGGTGGAGGCG 25
Db 23 CTAGACTGGACTGGGTAGTCG 2

RESULT 15
US-09-898-883-19
; Sequence 19, Application US/09898883
; Patent No. US20020164799A1
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,883
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
```

```

;
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-898-883-19

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Query Match      46.7%; Score 14; DB 9; Length 28;
Best Local Similarity 77.3%; Pred. NO. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      8 AATGAACGGTGAAGCGGCGAG 29
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Db      6 AATTAAGTGTGAAGCGGCGAG 27

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Job time : 92.1952 secs

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 2545.58 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30
Sequence: 1 GCTCTAGATGAACCGTGAAGCGGCAGG 30

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Maximum Match 100%
Listing first 45 summaries

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43: /cgn2_6/ptodata/2/pna/US08 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	30	9	US-08-510-736-5
3	30	100.0	30	11	US-08-770-564A-8
4	30	100.0	30	21	US-09-540-119B-10
5	30	100.0	30	28	US-09-717-828A-5
6	30	100.0	30	28	US-09-717-828B-5
7	30	100.0	30	28	US-09-717-829A-5
8	30	100.0	30	34	US-09-903-461-2
9	23	76.7	27	1	PCT-US97-23619-26
10	22	73.3	25	16	US-09-250-336A-4
11	22	73.3	25	25	US-09-642-177-4
12	22	73.3	26	1	PCT-US96-14679-27
13	22	73.3	26	1	PCT-US96-14679A-27
14	22	73.3	26	1	PCT-US99-03302-4
15	22	73.3	26	1	PCT-US99-07533-4
16	22	73.3	26	1	PCT-US99-07533-4
17	22	73.3	26	6	US-08-272-102-23
18	22	73.3	26	7	US-08-387-524-19
19	22	73.3	26	8	US-08-472-802A-34
20	22	73.3	26	8	US-08-472-802B-24
21	22	73.3	26	8	US-08-482-115A-23

Sequence 19, Appl
Sequence 41, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 312, Appl
Sequence 17, Appl
Sequence 598, Appl
Sequence 23, Appl
Sequence 2, Appl
Sequence 45, Appl
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Sequence 598, Appl
Sequence 598, Appl
Sequence 5, Appl
Sequence 598, Appl
Sequence 598, Appl
Sequence 9, Appl
Sequence 26, Appl
Sequence 312, Appl
Sequence 312, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1
PCT-US97-23619-8
; Sequence 8, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 21"
PCT-US97-23619-8
Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGGAGGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGGCGGCAGG 30
RESULT 2
US-08-510-736-5
; Sequence 5, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-510-736-5
Query Match 100.0%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGGAGGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGGCGGCAGG 30

RESULT 3

US-08-770-564A-8
; Sequence 8, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-8

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 4
US-09-540-119B-10
; Sequence 10, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-10

Query Match 100.0%; Score 30; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 5
US-09-717-828A-5
; Sequence 5, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-5

Query Match 100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 6
US-09-717-828B-5
; Sequence 5, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature

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; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828B-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30
   |||||
Db 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30

RESULT 7
US-09-717-829A-5
; Sequence 5, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30
   |||||
Db 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30

RESULT 8
US-09-903-461-2
; Sequence 2, Application US/09903461
; GENERAL INFORMATION:
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Garimella, Viswanadham
; TITLE OF INVENTION: Method of Detection by Enhancement of Silver Staining
; FILE REFERENCE: 00-1086-A
; CURRENT APPLICATION NUMBER: US/09/903,461
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/217,782
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 98.
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-09-903-461-2

Query Match      100.0%; Score 30; DB 34; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGGAGCGGCAGG 30

RESULT 9
PCT-US97-23619-26
; Sequence 26, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..27
; OTHER INFORMATION: /note= "hTR reverse primer"
PCT-US97-23619-26

Query Match      76.7%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAGG 23
```

Db 5 GCTCTAGATGAACGGTGAAG 27
|||||

RESULT 10
US-09-250-336A-4
; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 73.3%; Score 22; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
|||||

Db 4 GCTCTAGATGAACGGTGAAG 25
|||||

RESULT 11
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 73.3%; Score 22; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

Db 4 GCTCTAGATGAACGGTGAAG 25
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RESULT 12
PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
|||||

Db 5 GCTCTAGATGAACGGTGAAG 26
|||||

RESULT 13
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/14679A
FILING DATE: 13-SEP-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KASTER ESQ., KEVIN R.
REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 012/045PCT
TELEPHONE: (415) 473-7779
TELEFAX: (415) 473-7750
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGGGAAG 22
DB 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 14
PCT-US99-03302-4
; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
; FILE REFERENCE: 1489US 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGGGAAG 22
DB 5 GCTCTAGATGAACGGTGGGAAG 26

GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGGGAAG 22
DB 5 GCTCTAGATGAACGGTGGGAAG 26

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Job time : 2547.19 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 716.653 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTCTAGATGAACGGTGAAGCGGCGAGG 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
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- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	30	10	US-10-330-872A-5
3	23	76.7	23	1	PCT-US03-04088-520
4	22	73.3	23	1	PCT-US03-04088-529
5	22	73.3	26	6	US-09-721-456-598
6	22	73.3	26	9	US-10-325-810-598
7	22	73.3	26	9	US-10-359-935-23
8	21	70.0	21	1	PCT-US03-04088-587
9	21	70.0	23	1	PCT-US03-04088-521
10	20	66.7	21	1	PCT-US03-04088-592
11	19	63.3	19	1	PCT-US03-04088-14
12	19	63.3	19	1	PCT-US03-04088-257
13	19	63.3	19	1	PCT-US03-04088-278
14	19	63.3	21	1	PCT-US03-04088-538
15	19	63.3	21	1	PCT-US03-04088-539
16	19	63.3	21	1	PCT-US03-04088-542
17	19	63.3	21	1	PCT-US03-04088-543
18	19	63.3	21	1	PCT-US03-04088-546
19	19	63.3	21	1	PCT-US03-04088-547
20	19	63.3	21	1	PCT-US03-04088-550

21	19	63.3	21	1	PCT-US03-04088-551	Sequence 551, App
22	19	63.3	21	1	PCT-US03-04088-554	Sequence 554, App
23	19	63.3	21	1	PCT-US03-04088-555	Sequence 555, App
24	19	63.3	21	1	PCT-US03-04088-558	Sequence 558, App
25	19	63.3	21	1	PCT-US03-04088-559	Sequence 559, App
26	16.8	56.0	38	12	US-60-432-699-268	Sequence 268, App
27	16.4	54.7	18	6	US-09-721-456-543	Sequence 543, App
28	16.4	54.7	18	9	US-10-325-810-543	Sequence 543, App
29	16.2	54.0	25	9	US-10-355-577-381773	Sequence 381773, App
30	16.2	54.0	25	12	US-60-427-836-119888	Sequence 119888, App
31	16	53.3	25	12	US-60-417-190-121065	Sequence 121065, App
32	16	53.3	25	12	US-60-417-190-121066	Sequence 121066, App
33	16	53.3	25	13	US-60-470-475-106304	Sequence 106304, App
34	15.8	52.7	25	9	US-10-355-577-751232	Sequence 751232, App
35	15.8	52.7	30	9	US-10-213-926-31	Sequence 31, App
36	15.6	52.0	30	10	US-10-340-139-31	Sequence 31, App
37	15.6	52.0	25	7	US-09-954-445A-52770	Sequence 52770, App
38	15.6	52.0	25	12	US-60-427-808-483204	Sequence 483204, App
39	15.4	51.3	25	9	US-10-355-577-775297	Sequence 775297, App
40	15.4	51.3	25	9	US-10-355-577-775298	Sequence 775298, App
41	15.2	50.7	25	12	US-60-427-808-738286	Sequence 738286, App
42	15.2	50.7	50	1	PCT-US03-13015-881	Sequence 881, App
43	15.2	50.7	50	9	US-10-325-899-5782	Sequence 5782, App
44	15	50.0	25	9	US-10-355-577-906233	Sequence 906233, App
45	15	50.0	25	9	US-10-355-577-906236	Sequence 906236, App

ALIGNMENTS

RESULT 1
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGAGG 30
|||||
Db 1 GCTCTAGATGAACGGTGAAGCGGCGAGG 30
|||||

RESULT 2
US-10-330-872A-5
; Sequence 5, Application US/10330872A

OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 76.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAGG 23
Db 23 GCTCTAGATGAACGGTGGGAAGG 1

RESULT 4
PCT-US03-04088-529/c
Sequence 529, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent in version 3.2
SEQ ID NO 529
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
PCT-US03-04088-529

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGGGAAGCGGCAGG 30
Db 23 ATGAACGGTGGGAAGCGGCAGG 2

RESULT 5
US-09-721-456-598
Sequence 598, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727

OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 76.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAGG 23
Db 23 GCTCTAGATGAACGGTGGGAAGG 1

RESULT 4
PCT-US03-04088-529/c
Sequence 529, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent in version 3.2
SEQ ID NO 529
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
PCT-US03-04088-529

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGGGAAGCGGCAGG 30
Db 23 ATGAACGGTGGGAAGCGGCAGG 2

RESULT 5
US-09-721-456-598
Sequence 598, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727

1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598
Query Match 73.3%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGAAG 22
Db 5 GCTCTAGATGAACGGTGAAG 26
RESULT 6
US-10-325-810-598
SEQUENCE 598, Application US/10325810
GENERAL INFORMATION:

1
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGAAG 22
|||||

Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 7

US-10-359-935-23

Sequence 23, Application US/10359935

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

Feng, Junli

Funk, Walter

Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/359,935

APPLICATION NUMBER: US/10/359,935

FILING DATE: 07-Feb-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/057,351

FILING DATE: 08-APR-1994

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-359-935-23

Query Match

Best Local Similarity 73.3%; Score 22; DB 9; Length 26;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGAAG 22

Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 8

PCT-US03-04088-587/c

Sequence 587, Application PC/TUS0304088

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

SEQUENCE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

FILE REFERENCE: 02-708-A (400/080)

CURRENT APPLICATION NUMBER: PCT/US03/04088

CURRENT FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: US 60/396,600

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

NUMBER OF SEQ ID NOS: 626

SOFTWARE: PatentIn version 3.2

SEQ ID NO 587

LENGTH: 21

TYPE: RNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

OTHER INFORMATION: region

PCT-US03-04088-587

Query Match

Best Local Similarity 70.0%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGAACGGCGCAG 29

Db 21 ATGAACGGTGAACGGCGCAG 1

RESULT 9

PCT-US03-04088-521/c

Sequence 521, Application PC/TUS0304088

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

SEQUENCE OF INVENTION: Expression Using Short Interfering RNA (siNA)

FILE REFERENCE: 02-708-A (400/080)

CURRENT APPLICATION NUMBER: PCT/US03/04088

CURRENT FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: US 60/396,600

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

NUMBER OF SEQ ID NOS: 626

SOFTWARE: PatentIn version 3.2

SEQ ID NO 521

LENGTH: 23

TYPE: RNA

ORGANISM: Artificial


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;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match          70.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTGAACGGTGGAA 21
    |||||:|||||:|||||
Db 21 GCTCTAGAGTGAACGGTGGAA 1

RESULT 10
PCT-US03-04088-592
; Sequence 592, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
PCT-US03-04088-592

Query Match          66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 52;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGAAGCGGCAGG 30
    |||||:|||||:|||||
Db 1 GAACGGUGAAGCGGCAGG 20

RESULT 11
PCT-US03-04088-14/c
; Sequence 14, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
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;
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-14

Query Match          63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGAAGCGGC 27
    |||||:|||||:|||||
Db 19 ATGAACGGTGAAGCGGC 1

RESULT 12
PCT-US03-04088-257/c
; Sequence 257, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 257
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
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Fri Jun 27 07:43:13 2003

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; OTHER INFORMATION: region
PCT-US03-04088-257

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGCTGAAGCGGCAG 29
   |||||
Db 19 GAACGCTGAAGCGGCAG 1

RESULT 13
PCT-US03-04088-278
; Sequence 278, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGCTGAAGCGGC 27
   |||||
Db 1 AUGAACGUGGAGCGGC 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAACGGTGGA 21
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Db 19 TCTAGATGAACGGTGGA 1

RESULT 15
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
PCT-US03-04088-538
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; OTHER INFORMATION: Description of Artificial Sequence:  s1NA sense region
; FEATURE:
; NAME/KEY:  misc.feature
; LOCATION:  (20)..(21)
; OTHER INFORMATION:  n stands for thymidine
PCT-US03-04088-539
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Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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QY      1  GCTCTAGATGAACGGTGG 19
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Db      19  GCTCTAGATGAACGGTGG 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
Sequence: 1 CCAACTCTTCGGGTGGCAG 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AR063831	AR063831 Sequence
2	20	100.0	30	6	AR063829	AR063829 Sequence
3	13	65.0	46	6	I28704	I28704 Sequence 7
4	12	60.0	26	6	AX109246	AX109246 Sequence
5	11	55.0	20	6	A30766	A30766 Artificial
6	11	55.0	20	12	AB069392	AB069392 Synthetic
7	11	55.0	21	6	A37934	A37934 Sequence 12
8	11	55.0	24	6	AX445639	AX445639 Sequence
9	11	55.0	25	6	AX115384	AX115384 Sequence
10	11	55.0	30	6	AR142066	AR142066 Sequence
11	11	55.0	30	6	I59933	I59933 Sequence 60
12	11	55.0	30	6	I86791	I86791 Sequence 60
13	11	55.0	30	6	I95816	I95816 Sequence 60
14	11	55.0	36	6	AX060321	AX060321 Sequence
15	11	55.0	43	6	AX484473	AX484473 Sequence
16	11	55.0	48	6	AX068199	AX068199 Sequence
17	11	55.0	48	6	AX068203	AX068203 Sequence
18	10	50.0	11	6	I18772	I18772 Sequence 3
19	10	50.0	11	6	I95608	I95608 Sequence 3
20	10	50.0	15	6	AR056247	AR056247 Sequence
21	10	50.0	15	6	AR114005	AR114005 Sequence
22	10	50.0	18	6	AR008099	AR008099 Sequence
23	10	50.0	18	6	AX378621	AX378621 Sequence
24	10	50.0	20	4	BOVINE20	D83300 Bovine DNA
25	10	50.0	20	6	A30767	A30767 Artificial
26	10	50.0	20	6	AR063830	AR063830 Sequence
27	10	50.0	20	6	AR068779	AR068779 Sequence
28	10	50.0	20	6	AR092381	AR092381 Sequence
29	10	50.0	20	6	AR092653	AR092653 Sequence
30	10	50.0	20	6	AR130983	AR130983 Sequence
31	10	50.0	20	6	AR139457	AR139457 Sequence
32	10	50.0	20	6	AX293905	AX293905 Sequence
33	10	50.0	20	6	AX294358	AX294358 Sequence
34	10	50.0	20	6	AX294843	AX294843 Sequence
35	10	50.0	20	6	AX363221	AX363221 Sequence
36	10	50.0	20	6	E22563	E22563 Process for
37	10	50.0	20	6	E25721	E25721 Method for
38	10	50.0	20	12	AB069038	AB069038 Synthetic
39	10	50.0	21	6	AX033200	AX033200 Sequence
40	10	50.0	21	6	AX350215	AX350215 Sequence
41	10	50.0	22	4	DOGFP34801	L24234 Dog (Clone)
42	10	50.0	22	6	AX399648	AX399648 Sequence
43	10	50.0	22	6	AX399649	AX399649 Sequence
44	10	50.0	22	6	AX399650	AX399650 Sequence
45	10	50.0	23	6	AX253560	AX253560 Sequence

ALIGNMENTS

RESULT 1	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SRP-1999
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DEFINITION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SRP-1999
ACCESSION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SRP-1999
VERSION	AR063831.1	GI:5993139	20 bp	DNA	linear	PAT 29-SRP-1999
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.					
TITLE	Methods for detecting the RNA component of telomerase					
JOURNAL	Patent: US 5846723-A 7 08-DEC-1998;					
FEATURES	Location/Qualifiers					

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1. .20
/organism="unknown"
BASE COUNT 3 a 7 c 6 g 4 t
ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 0.13; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CCAACTCTTCGCGGTGGCAG 20
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Db 1 CCAACTCTTCGCGGTGGCAG 20
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RESULT 2
LOCUS AR063829 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5846723.
ACCESSION AR063829
VERSION AR063829.1 GI:5993137
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 5 08-DEC-1998;
FEATURES
    source 1. .30
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BASE COUNT 6 a 10 c 9 g 5 t
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Best Local Similarity 100.0%; Pred. NO. 0.13; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CCAACTCTTCGCGGTGGCAG 20
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Db 11 CCAACTCTTCGCGGTGGCAG 30
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RESULT 3
LOCUS I28704 46 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5573924.
ACCESSION I28704
VERSION I28704.1 GI:1819480
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Beckmann,M.Patricia., Goodwin,R.G., Giri,J.G. and Armitage,R.J.
TITLE CD27 ligand
JOURNAL Patent: US 5573924-A 7 12-NOV-1996;
FEATURES
    source 1. .46
    /organism="unknown"
BASE COUNT 6 a 12 c 14 g 14 t
ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 2.6e+03; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 3 AACTCTTCGCGGT 15
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Db 25 AACTCTTCGCGGT 37
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RESULT 4
LOCUS AX109246 26 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 13 from Patent WO0125269.
ACCESSION AX109246
VERSION AX109246.1 GI:13924119
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and Venema,J.
TITLE Human g-protein coupled receptor
JOURNAL Patent: WO 0125269-A 13 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
FEATURES
    Location/Qualifiers
    source 1. .26
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="Degenerated primers"
    variation 21
    /note="A,C,G or T"
    variation 24
    /note="A, C, G or T"
BASE COUNT 1 a 7 c 9 g 5 t 4 others
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Query Match 60.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. NO. 1.1e+04; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 6 TCTTCGCGGTGG 17
    |||||
Db 5 TCTTCGCGGTGG 16
    |||||

RESULT 5
LOCUS A30766 20 bp DNA linear PAT 24-JUL-1996
DEFINITION Artificial DNA for oligonucleotide (TB-5).
ACCESSION A30766
VERSION A30766.1 GI:1567066
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
    artificial sequences.
FEATURES
    Location/Qualifiers
    source 1. .20
    /organism="synthetic construct"
    /db_xref="taxon:32630"
BASE COUNT 2 a 11 c 4 g 3 t
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. NO. 4.6e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 10 CGCGGTGGCAG 20
    |||||
Db 11 CGCGGTGGCAG 1
    |||||

RESULT 6
LOCUS AB069392/c 20 bp DNA linear SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-stsG28879
    at ip36.
ACCESSION AB069392
VERSION AB069392.1 GI:15130196
KEYWORDS
SOURCE synthetic construct DNA.
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
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AUTHORS Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.

TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36.

JOURNAL Genomics 74 (1), 55-70 (2001)

MEDLINE 21269192

REFERENCE 2 (bases 1 to 20)

AUTHORS Horii, A.

TITLE Direct Submission

JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel: 81-22-717-8042, Fax: 81-22-717-8047)

FEATURES Location/Qualifiers

source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"

misc_feature 1..20
/note="forward primer for human STS sts-stSG28879 at 1p36 sts-stSG28879 obtained from clones B52P16, B32C18, B36214, Human BAC library RPCI-11"

BASE COUNT 4 a 4 c 5 g 7 t

ORIGIN

Query Match 55.0%; Score 11; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCCTCGCGGT 15
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DB 15 CTCCTCGCGGT 5

RESULT 7

LOCUS A37934 21 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 12 from Patent WO9408018.

ACCESSION A37934

VERSION A37934.1 GI:2294591

KEYWORDS unidentified.

SOURCE unidentified.
unclassified.

REFERENCE 1 (bases 1 to 21)
Varvill, K., Pickersgill, R.W., Gould, G.W., Goodenough, P.W. and Mosely, B.E.

AUTHORS ALTERATION OF POLYPEPTIDES

TITLE Patent: WO 9408018-A 12 14-APR-1994;
UNILEVER PLC (GB)

JOURNAL Other publication GB 2273931 940706
Other publication JP 8501939T 960305.

COMMENT Location/Qualifiers

FEATURES source 1..21
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 8 a 5 c 7 g 1 t

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCTTCGCGGTG 16
|||||

DB 19 TCTTCGCGGTG 9

RESULT 8

LOCUS AX445639/c 24 bp DNA linear PAT 03-JUL-2002

DEFINITION Sequence 2094 from Patent WO0216649.

ACCESSION AX445639

VERSION AX445639.1 GI:21692920

KEYWORDS synthetic construct.
synthetic construct.
artificial sequences.

ORGANISM 1

REFERENCE 1

AUTHORS Gunderson, K.

TITLE Probes and decoder oligonucleotides

JOURNAL Patent: WO 0216649-A 2094 28-FEB-2002;
Illumina, Inc. (US)

FEATURES Location/Qualifiers

source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

BASE COUNT 4 a 8 c 6 g 6 t

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCACTCTTCGC 12
|||||

DB 11 CCACTCTTCGC 1

RESULT 9

LOCUS AX115384 25 bp DNA linear PAT 11-MAY-2001

DEFINITION Sequence 507 from Patent WO0129262.

ACCESSION AX115384

VERSION AX115384.1 GI:14032326

KEYWORDS synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE 1 (bases 1 to 25)
Picoult-Newburg, L. and Pohl, M.

AUTHORS Genotyping reagents, kits and methods of use thereof

TITLE Patent: WO 0129262-A 507 28-APR-2001;
Orchid Biosciences, Inc. (US)

JOURNAL Location/Qualifiers

FEATURES source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 5 a 10 c 2 g 8 t

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACTCTTCG 11
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DB 12 CCACTCTTCG 22

RESULT 10

LOCUS AR142066/c 30 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 60 from patent US 6174668.

ACCESSION AR142066

VERSION AR142066.1 GI:15102366

KEYWORDS Unknown.
Unknown.

ORGANISM 1 (bases 1 to 30)
Cummins, T.J., Atwood, S. Melissa., Bergmeyer, L., Findlay, J. Bruce., Sutherland, J.W.H. and Kerschner, J.H.

REFERENCE 1 (bases 1 to 30)

AUTHORS

TITLE Diagnostic compositions, elements, methods and test kits for amplification and detection of two or more target DNA's using primers having matched melting temperatures

JOURNAL Patent: US 6174668-A 60 16-JAN-2001;

FEATURES Location/Qualifiers

source 1..30

BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 11

159933/c

LOCUS 30 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 60 from patent US 5654416.

ACCESSION 159933

VERSION 159933.1 GI:2478565

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce.,

Sutherland,J.W.H. and Kerschner,J.H.

TITLE Diagnostic primers and probes

JOURNAL Patent: US 5654416-A 60 05-AUG-1997;

FEATURES Location/Qualifiers

source 1..30

BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

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Best Local Similarity 100.0%; Pred. No. 4.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 12

186791/c

LOCUS 30 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 60 from patent US 5702901.

ACCESSION 186791

VERSION 186791.1 GI:3206509

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce.,

Sutherland,J.W.H. and Kerschner,J.H.

TITLE Diagnostic compositions, elements, methods and test kits for

amplification and detection of two or more DNA's using primers

having matched melting temperatures

Patent: US 5702901-A 60 30-DEC-1997;

FEATURES Location/Qualifiers

source 1..30

BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

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Best Local Similarity 100.0%; Pred. No. 4.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 13

195816/c

LOCUS 30 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 60 from patent US 5733751.

ACCESSION 195816

VERSION 195816.1 GI:3940286

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce.,

Sutherland,J.W.H. and Kerschner,J.H.

TITLE Diagnostic compositions, elements, methods and test kits for

amplification and detection of two or more DNA's using primers

having matched melting temperatures

Patent: US 5733751-A 60 31-MAR-1998;

FEATURES Location/Qualifiers

source 1..30

BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 20 CGCGGTGGCAG 30

Best Local Similarity 100.0%; Pred. No. 4.5e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 14

AX060321

LOCUS 36 bp DNA linear PAT 22-JAN-2001

DEFINITION Sequence 29 from Patent WO0078802.

ACCESSION AX060321

VERSION AX060321.1 GI:12405810

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 36)

AUTHORS Shinkets,R.A., Fernandes,E., Vernet,C., Yang,M., Boldog,F.L. and

Herrmann,J.L.

TITLE Secreted polypeptides and corresponding polynucleotides

JOURNAL Patent: WO 0078802-A 29 28-DEC-2000;

FEATURES Location/Qualifiers

source 1..36

BASE COUNT 7 a 12 c 12 g 5 t

ORIGIN /db_xref="taxon:32630"

/note="chemically synthesized"

Query Match 55.0%; Score 11; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 15

AX060321

LOCUS 36 bp DNA linear PAT 22-JAN-2001

DEFINITION Sequence 29 from Patent WO0078802.

ACCESSION AX060321

VERSION AX060321.1 GI:12405810

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 36)

AUTHORS Shinkets,R.A., Fernandes,E., Vernet,C., Yang,M., Boldog,F.L. and

Herrmann,J.L.

TITLE Secreted polypeptides and corresponding polynucleotides

JOURNAL Patent: WO 0078802-A 29 28-DEC-2000;

FEATURES Location/Qualifiers

source 1..36

BASE COUNT 7 a 12 c 12 g 5 t

ORIGIN /db_xref="taxon:32630"

/note="chemically synthesized"

Query Match 55.0%; Score 11; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 20 CGCGGTGGCAG 30


```

RESULT 15
AX484473
LOCUS AX484473 43 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1773 from Patent WO02053728.
ACCESSION AX484473
VERSION AX484473.1 GI:22318825
KEYWORDS
SOURCE
ORGANISM
Candida albicans.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
AUTHORS Gene disruption methodologies for drug target discovery
TITLE Patent: WO 02053728-A 1773 11-JUL-2002;
JOURNAL Elitra Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
1..43
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 18 a 8 c 7 g 10 t
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11
|||||
Db 28 CCAACTCTTCG 38

```

Search completed: June 23, 2003, 06:34:18
Job time : 235.051 secs

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```

XX OS Synthetic.
XX PN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-27948P.
XX PR 23-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes -
XX PS Claim 1; Page 189; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
XX SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAACTCTTCGC 12
Db 14 CAACTCTTCGC 24

Search completed: June 23, 2003, 05:43:37
Job time : 134.216 secs

```

CC employed to screen gene libraries to identify DKG reductases or cross
 CC reactive activities. DKGR nucleic acids may be sequenced and subjected to
 CC site specific mutagenesis to develop modified DKGR with desired
 CC properties that are absent or less pronounced in the wild-type proteins,
 CC such as greater catalytic efficiency, stability to heat, solvent
 CC tolerance, NADH dependent activity and different optimum pH. The sequence
 CC presented is the PCR primer, 28L5, used to amplify
 CC 2,5-diketo-D-gluconic acid reductase d (DKGRd) gene (clone pi-28) from
 CC DNA extracted from soil samples.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGT 15
 Db 10 CTCTTCGCGGT 20

RESULT 13
 ABQ02087/c
 ID ABQ02087 standard; DNA; 24 BP.

XX AC ABQ02087;

DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 2078.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting
 PT a target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes -

XX Claim 1; Page 93; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (I).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTCGC 12
 Db 11 CAACTCTTCGC 1

RESULT 14

ABQ08101/c
 ID ABQ08101 standard; DNA; 24 BP.

XX AC ABQ08101;

XX 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 8092.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting
 PT a target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes -

XX Claim 1; Page 189; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (I).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTCGC 12
 Db 11 CAACTCTTCGC 1

RESULT 15

ABQ08142
 ID ABQ08142 standard; DNA; 24 BP.

XX AC ABQ08142;

XX 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 8133.

XX Oligonucleotide array; adapter sequence; probe; ss.

PF 28-SEP-1993; 93WO-GB02026.
 XX
 PR 28-SEP-1992; 92GB-0020418.
 XX
 XX (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 XX
 XX Goodenough PW, Gould WM, Moseley BEE, Pickersgill RW;
 PI Varhill K, Gould GW, Moseley BEB, Varvill K;
 XX WPI; 1994-135584/16.
 DR
 XX Preparation of new reduced size polypeptide(s), partic. enzyme(s)
 PT - lacking at least a part of a loop region while retaining
 PT biologically functional activity
 XX
 PS Disclosure; Page 26; 59pp; English.
 XX
 CC This sequence verified a Cys to Thr mutation had occurred
 CC at a position equivalent to codon 94 of a truncated hen egg white
 CC lysozyme gene following site-directed mutagenesis via inverse PCR
 CC using an oligonucleotide
 CC DNA primer (AA062039).
 XX
 XX Sequence 21 BP; 8 A; 5 C; 7 G; 1 T; 0 other;
 Query Match 55.0%; Score 11; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TCTTCGGGTG 16
 DB 19 TCTTCGGGTG 9
 RESULT 11
 AAC68689/c
 ID AAC68689 standard; DNA; 22 BP.
 XX
 AC AAC68689;
 XX
 XX 22-FEB-2001 (first entry)
 DT
 DE Mouse R35 specific primer MM-R35-EUL.
 XX
 XX Mouse; R35; uropathic; antiinflammatory; analgesic;
 KW gene therapy; seven transmembrane receptor; neuropathic pain;
 KW inflammation; incontinence; irritable bowel syndrome;
 KW PCR primer; ss.
 XX
 XX Mus musculus.
 OS
 XX
 XX WO200064928-A2.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 20-APR-2000; 2000WO-GB01546.
 PF
 XX
 XX 21-APR-1999; 99GB-0009161.
 PR
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (PLAC) MAX-PLANCK INST NEUROBIOLOGY.
 XX
 XX Barde Y, Friedel R, Michalovich D, Reith AD, Schnuerch H;
 PI Stubbusch J;
 XX
 XX WPI; 2000-679669/66.
 DR
 XX Novel R35 polypeptides and polynucleotides useful for treating
 PT neuropathic, inflammatory and chronic pain, incontinence and irritable
 PT bowel syndrome -
 XX
 PS Example 4; Page 25; 55pp; English.

XX The present sequence was used in the cloning of full-length mouse R35
 CC cDNA. R35 is a seven transmembrane receptor which is useful for
 CC treating neuropathic pain, inflammatory and chronic pain, incontinence,
 CC and disorders of the gastrointestinal tract associated with gut motility
 CC and secretion such as irritable bowel syndrome. It is also useful for
 CC inducing an immune response in a mammal to protect against the diseases.
 CC It is useful in screening assays to identify compounds which stimulate or
 CC inhibit the function of the polypeptide, to identify membrane bound or
 CC soluble receptors and also for the structure-based design of an agonist,
 CC antagonist or inhibitor of R35.
 XX
 XX Sequence 22 BP; 8 A; 5 C; 7 G; 2 T; 0 other;
 Query Match 55.0%; Score 11; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CTCCTCGCGGT 15
 DB 14 CTCCTCGCGGT 4
 RESULT 12
 ABK86775
 ID ABK86775 standard; DNA; 22 BP.
 XX
 AC ABK86775;
 XX
 XX 24-SEP-2002 (first entry)
 DT
 XX
 DE PCR primer, 28L5, used to amplify 2,5 DKG reductase d (clone pi-28).
 KW 2,5-diketo-D-gluconic acid reductase d; DKGRd; aldo-keto reductase;
 KW glucose; ascorbic acid; 2-keto-L-gulonic acid; vitamin C; immunogen;
 KW catalytic efficiency; thermal stability; solvent tolerance; pH optimum;
 KW PCR; primer; ss; pi-28.
 XX
 XX Unidentified.
 OS
 XX WO200229019-A2.
 PN
 XX
 XX 11-APR-2002.
 PD
 XX
 XX 02-OCT-2001; 2001WO-US42445.
 PF
 XX
 XX 04-OCT-2000; 2000US-0684385.
 PR
 XX
 XX (GEMV) GENENCOR INT INC.
 PA
 XX
 XX Donnelly M, Eichenfeldt WH, Trent J;
 PI
 XX WPI; 2002-463231/49.
 DR
 XX
 XX Diketo-D-gluconic acid reductases, isolated from the environment using
 PT polymerase chain reaction methods, useful to provide new catalysts with
 PT desirable traits for industrial processes -
 XX
 XX Example 1; Page 31; 58pp; English.
 PS
 XX The invention discloses the isolated polypeptide, and polynucleotide
 CC encoding it, 2,5-diketo-D-gluconic acid reductase (DKGR) which is a
 CC member of the aldo-keto reductase superfamily. The reductase, in
 CC particular in Pantoea sp., is useful for converting glucose to ascorbic
 CC acid, by culturing the host cell under conditions suitable for the
 CC expression of DKGR. Glucose is first converted to 2,5-diketo-D-gluconic
 CC acid by endogenous oxidases and this is then reduced enzymatically to
 CC 2-keto-L-gulonic acid by a heterologous DKGR expressed in the production
 CC strain of bacteria. DKGR nucleic acids and proteins are useful to make
 CC enzymes useful in industrial processes to convert glucose to vitamin C in
 CC a single organism. DKGR proteins or their fragments and derivatives are
 CC useful as immunogens to produce antibodies useful in screening for
 CC similar enzymes from other organisms and samples. These antibodies are

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XX AAQ22888;
XX
XX 07-JUL-1992 (first entry)
XX
XX HCV-Hc59 primer #626 (sense strand).
XX
XX Hepatitis C virus; non-A non-B virus; HCV-Hc59; primers;
XX probes; vaccine; ss.
XX
XX Synthetic.
XX
XX WO9203458-A.
XX
XX 05-MAR-1992.
XX
XX 23-AUG-1991; 91WO-US06037.
XX
XX 21-NOV-1990; 90US-0616369.
XX
XX 25-AUG-1990; 90US-0573643.
XX
XX (NYBL-) NEW YORK BLOO DCENT.
XX
XX (PHAA ) PHARMACIA GENETIC ENG INC.
XX
XX Zebedee S, Inchauspe G, Nasofe MS, Prince AM;
XX
XX WPI; 1992-096821/12.
XX
XX Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
XX virus - obt'd. Hutch C59 subgroup encoding polypeptide(s), useful
XX as vaccines, and immuno reactive Abs for diagnosis of virus
XX
XX Disclosure; Page 107; 225pp; English.
XX
XX One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate
XX (HCV-Hc59) was propagated through passage in animals and the
XX entire viral genome was cloned and sequenced.
XX Five microg of purified liver or plasma derived from HCV RNA was
XX used per cDNA priming reaction. Specific nucleotide primers
XX derived from published HCV sequences and spanning the entire
XX reported genomic sequences were used to prime the reaction.
XX Selected target sequences were amplified using a PCR-based approach
XX using a variety of nucleotide primers. The nucleotide sequences
XX of the primers are given in AAQ22872-936 and AAQ24472. Amplified
XX sequences were subsequently isolated, rendered blunt-ended and
XX inserted into a pUC or pBluescript cloning vectors.
XX
XX Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 other;
XX
XX Query Match 55.0%; Score 11; DB 13; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.8e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 ACTCTTCGCGG 14
XX | | | | |
XX 11 ACTCTTCGCGG 1
XX
XX Db
XX
XX RESULT 9
XX ABL43707/c
XX ID ABL43707 standard; DNA; 20 BP.
XX
XX AC ABL43707;
XX
XX 11-APR-2002 (first entry)
XX
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:751.
XX
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX genome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2001321190-A.

```

```

XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-0068285.
XX
XX 10-MAR-2000; 2000JP-0066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones -
XX
XX Claim 4; Page 19; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
XX
XX Query Match 55.0%; Score 11; DB 24; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.8e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 CTCCTTCGCGGT 15
XX | | | | |
XX 15 CTCCTTCGCGGT 5
XX
XX Db
XX
XX RESULT 10
XX AAQ62049/c
XX ID AAQ62049 standard; DNA; 21 BP.
XX
XX AC AAQ62049;
XX
XX 09-OCT-1994 (first entry)
XX
XX DE Hen egg white lysozyme gene Cys to Thr mutation at codon 94.
XX
XX KW Hen egg white; lysozyme; enzyme engineering; protein engineering
XX fowl; plasmid pKP1500; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 10..12
XX /*tag= a
XX /note= "Cys to Thr mutation"
XX
XX WO9408018-A.
XX
XX 14-APR-1994.
XX
XX

```

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABP0010-ABP99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 other;

Query Match 55.0%; Score 11; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTGGC 12

Db 2 CAACTCTTGGC 12

RESULT 6

AA000290/c
 ID AAX00290 standard; DNA; 13 BP.

XX AC AAX00290;

XX 25-MAR-1999 (first entry)

DE Target DNA sequence DNA 6.

XX Melting point; temperature; nucleic acid; fluorescent intensity;
 KW probe; fluorescent intercalative dye; target DNA; diagnosis;
 KW detection; genetic mutation; homology; ss.

XX Synthetic.

XX EP892071-A2.

XX 20-JAN-1999.

XX 05-JUN-1998; 98EP-0304458.

XX 05-JUN-1997; 97JP-0147825.

XX (TOYU) TOSOH CORP.

XX Ishiguro T, Saitoh J;

XX WPI; 1999-083587/08.

XX Measuring melting temperature of nucleic acid - comprises monitoring
 PT fluorescent intensity of mixture of sample and fluorescently
 PT labelled probe

PS Example 3; Page 7; 24pp; English.

XX A method has been developed of measuring the melting temperature of a
 CC nucleic acid. The method comprises monitoring the fluorescent intensity
 CC of a mixture of a sample and a probe labelled with a fluorescent
 CC intercalative dye at different temperatures. The probe contains a base
 CC sequence complementary to a specific nucleic acid in the sample. The
 CC method is useful for clinical gene diagnosis by exploring unknown genes.
 CC It is useful for evaluating the homology of an unknown gene with a
 CC control gene sequence and as a method of detecting genetic mutations
 CC e.g. therapy for hepatitis C virus (HCV). The method is quicker and
 CC requires less labour as it specifically detects and quantifies the
 CC hybrid in a simple one-step measurement without requiring the separation
 CC of excess unhybridised probe. The method is more sensitive and can

CC detect small amounts of nucleic acids in sample e.g. tens of copies of
 CC target nucleic acids can be amplified to several ng. The present
 CC sequence represents a target DNA sequence from an example of the present
 CC invention.

XX Sequence 13 BP; 2 A; 5 C; 5 G; 1 T; 0 other;

Query Match 55.0%; Score 11; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCGCGGTGGCA 19

Db 12 TCGCGGTGGCA 2

RESULT 7

AA006516/c
 ID AAQ06516 standard; DNA; 20 BP.

XX AC AAQ06516;

DT 22-FEB-1991 (first entry)

DE Probe/primer TB-5 derived from mycobacterial gene.

XX mycobacterial antigen; actinomycetales; tuberculosis; ss.

XX Synthetic.

XX WO9012875-A.

XX 01-NOV-1990.

XX 13-APR-1990; 90WO-FR00274.

XX 17-APR-1989; 89FR-0005057.

XX (INRM) INSERM INST NAT SANTE.

XX (INSP) INST PASTEUR.

XX Hance A, Grandchamp-Desraux B, Levy-Frebault V, Gicouel B;

XX WPI; 1990-348478/46.

XX Nucleotide sequences of actinomycetales - used as primers for
 PT synthesis of DNA of actinomycetales

XX Claim 24; Page 39; 61pp; French.

XX This sequence is based on a fragment of a mycobacterial gene which
 CC encodes a protein homologous to the 65KD antigen of mycobacterium.
 CC TB-5 is used in a pair as a primer to amplify
 CC mycobacterial genes to detect mycobacteria. The oligonucleotide can
 CC also be used as a labelled probe to detect amplified mycobacterial
 CC sequences. It reacts specifically with Mycobacterium avium DNA.
 CC See also AAQ06505-Q06515, AAQ06517-Q06523 and AAR08336.

XX Sequence 20 BP; 2 A; 11 C; 4 G; 3 T; 0 other;

Query Match 55.0%; Score 11; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 11 CGCGGTGGCAG 1

RESULT 8

AAQ22888/c
 ID AAQ22888 standard; DNA; 20 BP.

XX

```

XX PI Cosman DJ, Dower SK, Lupton SD, Mosley BA, Sims JR;
XX WPI; 1998-361746/31.
XX
XX Regulation of interleukin-1 mediated immune or inflammatory response
XX in mammal - comprises administering soluble IL-1 receptor protein,
XX used in treatment of e.g. graft versus host disease and multiple
XX sclerosis
XX
XX Example 1; Column 19; 33pp; English.
XX
XX RAV34748-V34756 are primers used in the isolation of human and mouse
XX type II interleukin-1 receptor (IL-1R) which is used in a method to
XX investigate the regulation of the immune or inflammatory response in a
XX mammal. This method involves administering a soluble type-II IL-1
XX receptor protein in an amount effective to bind to IL-1 and prevent its
XX binding to cell-surface IL-1 receptors. The process can be used for
XX treating alloantigen-induced rejection of transplanted tissues or
XX organs, graft-versus-host disease and autoimmune dysfunction dependent
XX upon the activation of T cells against self antigens, selected from
XX rheumatoid arthritis, diabetes mellitus or multiple sclerosis.
XX
XX Sequence 46 BP; 6 A; 12 C; 14 G; 14 T; 0 other;
XX
XX Query Match 65.0%; Score 13; DB 19; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;
XX Matches 13; Conservative 0; Indels 0;
XX
XX QY 3 AACTCTTCGCGGT 15
XX | | | | | | | | | |
XX Db 25 AACTCTTCGCGGT 37
XX
XX RESULT 4
XX AAF80328
XX ID AAF80328 standard; DNA; 26 BP.
XX AC AAF80328;
XX
XX 29-JUN-2001 (first entry)
XX
XX PCR primer for cDNA encoding the G-protein coupled receptor IGS4.
XX
XX Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;
XX nervous system disorder; psychiatric disorder; Parkinson's disease;
XX episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke;
XX cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
XX motility disorder; myocardial infarction; hypertension; dyslipidemia;
XX gastrointestinal disorder; inflammatory bowel disease; osteoporosis;
XX inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
XX gynecological disorder; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200125269-A2.
XX
XX 12-APR-2001.
XX
XX 25-SEP-2000; 2000WO-EP09584.
XX
XX 24-SEP-1999; 99EP-0203140.
XX 24-SEP-1999; 99NL-1013140.
XX 28-JUL-2000; 2000EP-0202683.
XX 31-JUL-2000; 2000US-0222047.
XX
XX (SOLV ) SOLVAY PHARM BV.
XX
XX Deleersnijder W, Berger C, Loeken C, Nys G, Venema J;
XX WPI; 2001-273568/28.
XX
XX New G-protein coupled receptors and the polynucleotides encoding them,

```

```

PT useful for preventing, ameliorating or correcting nervous system
PT disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
PT or cancers
XX
XX Example 1a; Page 39; 102pp; English.
XX
XX PCR primers AAF80328-30 were used to amplify cDNA encoding a
XX human G-protein coupled receptor designated IGS4. IGS4 exists in two
XX polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
XX polynucleotides are useful for preventing, ameliorating or correcting
XX dysfunctions or diseases. These diseases include peripheral nervous
XX system, psychiatric and central nervous system disorders
XX (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's
XX disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases
XX (e.g. heart failure, angina pectoris, myocardial infarction or
XX hypertension), dyslipidemias, obesity, emesis, gastrointestinal
XX disorders (e.g. inflammatory bowel disease or motility disorders),
XX osteoporosis, inflammations, infections (e.g. bacterial, fungal,
XX protozoan or viral), pain, cancers, immune disorders, allergies,
XX sepsis or gynecological disorders. Agonists or antagonists of IGS4 are
XX effective with regard to disorders of the nervous system, including the
XX central and peripheral nervous systems, disorders of the gastrointestinal
XX system, cardiovascular system, skeletal muscle, thyroid, lung or
XX genitourinary system, or immunological disease. The IGS4 polynucleotides
XX are useful as diagnostic reagents for detecting under-expression,
XX overexpression or altered expression of IGS4.
XX
XX Sequence 26 BP; 1 A; 7 C; 9 G; 5 T; 4 other;
XX
XX Query Match 60.0%; Score 12; DB 22; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02; Mismatches 0; Gaps 0;
XX Matches 12; Conservative 0; Indels 0;
XX
XX QY 6 TCTTCGCGGTGG 17
XX | | | | | | | | | |
XX Db 5 TCTTCGCGGTGG 16
XX
XX RESULT 5
XX ABI41062
XX ID ABI41062 standard; DNA; 12 BP.
XX AC ABI41062;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 341035 for detecting SNP TSC0010735.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status
XX
XX Claim 1; SEQ ID 341035; 29pp + Sequence Listing; German.

```


XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;
Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CCAACTCTTCGGGTGGCAG 20
Db 1 CCAACTCTTCGGGTGGCAG 20
RESULT 2
AAV41172
ID AAV41172 standard; DNA; 30 BP.
XX
AC AAV41172;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 16.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN W09828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX

PT New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
Query Match 100.0%; Score 20; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CCAACTCTTCGGGTGGCAG 20
Db 11 CCAACTCTTCGGGTGGCAG 30
RESULT 3
AAV34750
ID AAV34750 standard; DNA; 46 BP.
XX
AC AAV34750;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human Type II IL-1R primer #3.
XX
KW Type II interleukin-1 receptor; IL-1R; immune response; inflammation;
KW regulation; soluble; cell surface receptor; treatment; alloantigen;
KW tissue; organ; rejection; transplant; graft-versus-host disease; human;
KW autoimmune dysfunction; T-cell activation; self antigen; primer;
KW rheumatoid arthritis; diabetes mellitus; multiple sclerosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN US5767064-A.
XX
PD 16-JUN-1998.
XX
PF 16-MAY-1995; 95US-0442043.
XX
PR 16-MAY-1991; 91US-0701415.
PR 05-JUN-1990; 90US-0534193.
PR 24-AUG-1990; 90US-0573576.
PR 13-DEC-1990; 90US-0627071.
PR 12-JUL-1993; 93US-0091519.
PR 13-MAY-1994; 94US-0242211.
PR 16-MAY-1995; 95US-0442043.
XX
PA (IMMV) IMMUNEX CORP.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20

Sequence: 1 CCAACTCTTCGGGTGGCAG 20

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	19 AAV41174	RNA component of h
2	20	100.0	30	19 AAV41172	RNA component of h
3	13	65.0	46	19 AAV4750	Human Type II IL-1
4	12	60.0	26	22 AAF80328	PCR primer for CDN
5	11	55.0	12	23 ABI1062	Oligonucleotide pr
6	11	55.0	13	20 AAX00290	Target DNA sequenc
c	7	11	55.0	13 AAO06516	Probe/primer TB-5
c	8	11	55.0	20 11 AAO22888	HCV-Hc5 primer #6
c	9	11	55.0	20 24 ABL43707	Human chromosome 1

c	10	11	55.0	21	15	AAQ62049	Hen egg white lyso
c	11	11	55.0	22	21	ABC68689	Mouse R35 specific
c	12	11	55.0	22	24	ABK67775	PCR primer, 28L5,
c	13	11	55.0	24	24	ABQ02087	Oligonucleotide ad
c	14	11	55.0	24	24	ABQ08101	Oligonucleotide ad
c	15	11	55.0	24	24	ABQ08142	Oligonucleotide ad
c	16	11	55.0	25	22	AAH37711	SNP specific SNPE
c	17	11	55.0	28	20	AZ229951	PCR primer DYV-218
c	18	11	55.0	36	22	AAH15371	Oligo 5R, to const
c	19	11	55.0	36	22	AAH15371	Human SEC2 DNA amp
c	20	11	55.0	37	19	AAV24106	Primer for T7 gene
c	21	11	55.0	37	19	AAV24106	Murine insulin-like
c	22	11	55.0	48	22	AAH67727	Rat insulin-like g
c	23	10	50.0	10	22	AAH67727	Yeast NORF gene SA
c	24	10	50.0	10	22	AAH67727	Oligonucleotide pr
c	25	10	50.0	12	23	AB119475	Oligonucleotide pr
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c	27	10	50.0	12	23	AB154849	Oligonucleotide pr
c	28	10	50.0	12	23	AB181242	Oligonucleotide pr
c	29	10	50.0	13	23	ABC17514	Oligonucleotide SE
c	30	10	50.0	13	23	ABC17515	Oligonucleotide SE
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c	33	10	50.0	13	23	ABF47778	Oligonucleotide SE
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c	36	10	50.0	13	23	ABH33140	Oligonucleotide SE
c	37	10	50.0	13	23	ABH33141	Oligonucleotide SE
c	38	10	50.0	15	16	AAH52289	Mouse ICAM hammerh
c	39	10	50.0	18	12	AAQ13542	Probe JFL330 to co
c	40	10	50.0	18	17	AAQ13542	Primer for detecti
c	41	10	50.0	18	17	AAQ13542	Primer for detecti
c	42	10	50.0	18	19	AAV08260	PCR primer ABCR, EX
c	43	10	50.0	18	21	AAA30862	Fragment of a plas
c	44	10	50.0	18	24	ABK41162	Human obesity-asso
c	45	10	50.0	19	19	AAV46209	Human HLA-A primer

ALIGNMENTS

RESULT 1

AAV41174

ID AAV41174 standard; DNA; 20 BP.

XX AAV41174;

XX AAV41174;

XX 08-OCT-1998 (first entry)

XX RNA component of human telomerase (htr) antisense oligo 16bc.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; htr;
XX immune system down-regulation; anti-inflammatory therapy; ss.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
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Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

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Maximum DB seq length: 50

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-08-770-565-7
2	20	100.0	30	2	US-08-770-565-5
3	14	70.0	45	6	5198342-4
4	13	65.0	46	1	US-08-091-519-5
5	13	65.0	46	1	US-08-106-507-7
6	13	65.0	46	1	US-08-442-043A-5
7	13	65.0	46	5	PCT-US91-03478-5
8	11	55.0	20	2	US-08-473-020A-13
9	11	55.0	30	1	US-08-495-743-60
10	11	55.0	30	1	US-08-495-739-60
11	11	55.0	30	1	US-08-495-741-60
12	11	55.0	30	4	US-08-062-023-60
13	11	55.0	38	1	US-08-664-449-61
14	10	50.0	11	1	US-07-778-233B-3
15	10	50.0	11	1	US-07-963-321-3
16	10	50.0	11	1	US-08-390-641-3
17	10	50.0	11	1	US-08-548-540-3
18	10	50.0	11	5	PCT-US96-09809-3
19	10	50.0	15	2	US-08-292-620A-451
20	10	50.0	15	3	US-09-071-845-451
21	10	50.0	18	1	US-08-599-252-1
22	10	50.0	18	1	US-08-436-074-1
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25	10	50.0	20	2	US-08-770-565-6
26	10	50.0	20	2	US-08-578-551-10
27	10	50.0	20	2	US-08-473-020A-14

c 28	10	50.0	20	2	US-09-289-368-52	Sequence 52, Appl
c 29	10	50.0	20	2	US-09-190-982-10	Sequence 10, Appl
c 30	10	50.0	20	4	US-09-408-257-10	Sequence 10, Appl
c 31	10	50.0	20	4	US-09-136-411-7	Sequence 7, Appl
c 32	10	50.0	20	4	US-09-472-035A-12	Sequence 12, Appl
c 33	10	50.0	20	4	US-09-545-686-26	Sequence 26, Appl
c 34	10	50.0	20	4	US-09-291-541-5	Sequence 5, Appl
c 35	10	50.0	21	4	US-09-338-907-420	Sequence 420, App
c 36	10	50.0	21	4	US-09-218-207-420	Sequence 420, App
c 37	10	50.0	21	4	US-09-291-541-2	Sequence 2, Appl
c 38	10	50.0	24	1	US-08-203-905B-25	Sequence 25, Appl
c 39	10	50.0	26	1	US-08-318-193-28	Sequence 28, Appl
c 40	10	50.0	26	1	US-08-318-193-29	Sequence 29, Appl
c 41	10	50.0	26	4	US-09-224-426-5	Sequence 5, Appl
c 42	10	50.0	26	4	US-09-478-601-5	Sequence 5, Appl
c 43	10	50.0	26	4	US-09-478-602-5	Sequence 5, Appl
c 44	10	50.0	28	1	US-07-844-297-5	Sequence 5, Appl
c 45	10	50.0	28	1	US-07-681-703B-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-7

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Best Local Similarity 100.0%; Pred. No. 0.0018;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCAACTCTTCGGCGTGGCAG 20

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; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5

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Db 11 CCAACTCTTCGGTGGCAG 30

RESULT 3
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; Patent No. 5198342
; APPLICANT: MALIISZEWSKI, CHARLES R.
; TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/548,059
; FILING DATE: 05-JUL-1990
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; LENGTH: 45

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Best Local Similarity 100.0%; Pred. No. 6.8;

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; Sequence 5, Application US/08091519
; Patent No. 5350683
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
US-08-091-519-5

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGT 15
Db 25 AACTCTTCGGGT 37

RESULT 5
US-08-106-507-7
; Sequence 7, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
US-08-106-507-7

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGT 15
Db 25 AACTCTTCGGGT 37

RESULT 6
US-08-442-043A-5
; Sequence 5, Application US/08442043A
; Patent No. 5767064
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,043A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-442-043A-5

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGT 15
Db 25 AACTCTTCGGGT 37

RESULT 7
PCT-US91-03478-5
; Sequence 5, Application PC/TUS9103478
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

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STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03478
FILING DATE: 19910517
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 06-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
PCT-US91-03478-5

Query Match 65.0%; Score 13; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
    |||||
Db 25 AACTCTTCGCGGT 37

RESULT 8
US-08-473-020A-13/c
; Sequence 13, Application US/08473020A
; Patent No. 587273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desaux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Gicquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; applications to the synthesis or detection of nucleic
; acids, products of expression of such sequences and
; application as immunogenic compositions.
; TITLE OF INVENTION: acids, products of expression of such sequences and
; application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,020A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-473-020A-13

Query Match 55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
    |||||
Db 11 CGCGGTGGCAG 1

RESULT 9
US-08-495-743-60/c
; Sequence 60, Application US/08495743
; Patent No. 565416
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Cummins, Susan M. Atwood
; APPLICANT: Lynn Bergmeyer, John B. Findlay
; APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner
; TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENTS,
; METHODS AND TEST KITS FOR
; TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF TWO
; OR MORE TARGET DNA'S USING PRIMERS
; TITLE OF INVENTION: HAVING MATCHED MELTING TEMPERATURES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Kodak Company, Patent Legal Staff
; STREET: 343 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14650 - 2201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: PC-8 (Word for Windows)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,743
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,023
; FILING DATE: 14-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tucker, J. Lanny
; REGISTRATION NUMBER: 27,678
; REFERENCE/DOCKET NUMBER: 67271A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 722-9332
; TELEFAX: (716) 477-4646
```


Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
|||||
Db 21 CGCGGTGGCAG 11

RESULT 12

US-08-062-023-60/c
; Sequence 60, Application US/08062023
; Patent No. 6174668
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Cummins, Susan M. Atwood
; APPLICANT: Lynn Bergmeyer, John B. Findlay
; APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner
; TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENTS,
; TITLE OF INVENTION: METHODS AND TEST KITS FOR
; TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF TWO
; TITLE OF INVENTION: OR MORE TARGET DNA'S USING PRIMERS
; TITLE OF INVENTION: HAVING MATCHED MELTING TEMPERATURES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Kodak Company, Patent Legal Staff
; STREET: 343 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14650 - 2201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: PC-8 (Word for Windows)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,023
; FILING DATE: 19930514
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tucker, J. Lanny
; REGISTRATION NUMBER: 27,678
; REFERENCE/DOCKET NUMBER: 67271A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 722-9332
; TELEFAX: (716) 477-4646
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Probe for Mycobacterium
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE: Synthetically prepared
; IMMEDIATE SOURCE: Same
; PUBLICATION INFORMATION: Unknown
US-08-062-023-60

Query Match 55.0%; Score 11; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
|||||
Db 21 CGCGGTGGCAG 11

RESULT 13

US-08-664-449-61/c

; Sequence 61, Application US/08664449
; Patent No. 5766905
; GENERAL INFORMATION:
; APPLICANT: Studier, F. W.
; APPLICANT: Rosenberg, Alan H.
; TITLE OF INVENTION: Cytoplasmic Bacteriophage Display System
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET: Building 902C
; CITY: Upton
; STATE: NY
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,449
; FILING DATE: 17-June-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AUI-9618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-7338
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-664-449-61

Query Match 55.0%; Score 11; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
|||||
Db 16 CGCGGTGGCAG 6

RESULT 14

US-07-778-233B-3/c
; Sequence 3, Application US/0778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,233B
; FILING DATE: 19911016

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-778-233B-3

Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCA 19
|||||||
Db 10 CGCGGTGGCA 1

RESULT 15

US-07-963-321-3/c
Sequence 3, Application US/07963321
Patent No. 538665
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,321
FILING DATE: 19921015
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,223
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-963-321-3

Query Match 50.0%; Score 10; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCA 19
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Db 10 CGCGGTGGCA 1

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Job time : 32.3147 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGCGAG 20

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OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

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Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
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- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	65.0	46	9	US-10-199-209-5
2	12	60.0	25	9	US-10-098-263B-31566
3	11	55.0	24	9	US-09-940-185-2094
4	11	55.0	25	9	US-10-098-263B-97446
5	11	55.0	25	9	US-10-098-263B-110352
6	11	55.0	25	9	US-10-098-263B-129624
7	11	55.0	36	8	US-08-961-888-12
8	11	55.0	36	9	US-10-002-050-29
9	11	55.0	36	9	US-10-002-304-29
10	11	55.0	36	12	US-10-003-152-29
11	10	50.0	20	9	US-09-971-894-12
12	10	50.0	20	10	US-09-909-849-17
13	10	50.0	21	9	US-09-853-526-420
14	10	50.0	21	10	US-09-901-484A-420
15	10	50.0	22	9	US-09-487-318-11
16	10	50.0	22	10	US-09-930-251-16
17	10	50.0	22	10	US-09-930-251-17
18	10	50.0	22	10	US-09-930-251-18
19	10	50.0	24	12	US-10-077-894-20

ALIGNMENTS

RESULT 1

US-10-199-209-5

; Sequence 5, Application US/10199209

; Publication No. US20030060616A1

; GENERAL INFORMATION:

; APPLICANT: Sims, John E.

; Cosman, David J.

; Lupton, Stephen D.

; Mosley, Bruce A.

; Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/199,209

; FILING DATE: 19-Jul-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/461,908

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/091,519

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/07/701,415

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 07/534,193

; FILING DATE: 06-JUN-1990

; APPLICATION NUMBER: US 07/573,576

; FILING DATE: 24-AUG-1990

; APPLICATION NUMBER: US 07/627,071

; FILING DATE: 13-DEC-1990

; ATTORNEY/AGENT INFORMATION:

Sequence 11414, A
Sequence 26951, A
Sequence 42033, A
Sequence 42034, A
Sequence 72819, A
Sequence 89453, A
Sequence 89454, A
Sequence 95961, A
Sequence 97445, A
Sequence 98053, A
Sequence 98054, A
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Sequence 16, Appli
Sequence 5, Appli
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Sequence 9, Appli

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25 9 US-10-098-263B-118620
25 9 US-10-098-263B-130018
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26 9 US-09-899-732-5
26 10 US-09-118-276-16
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27 10 US-09-824-984-9
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27 10 US-09-825-247A-9
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C 33
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C 37
C 38
C 39
C 40
C 41
C 42
C 43
C 44
C 45

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; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5
Query Match 65.0%; Score 13; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

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RESULT 2
US-10-098-263B-31566
; Sequence 31566, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-31566
Query Match 60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TCTTCGCGGTGG 17
Db 5 TCTTCGCGGTGG 16

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RESULT 3
US-09-940-185-2094/C
; Sequence 2094, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2094
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2094
Query Match 55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCAACTCTTCGC 12
Db 11 CCAACTCTTCGC 1

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```

RESULT 4
US-10-098-263B-97446
; Sequence 97446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-97446
Query Match 55.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTCTTCGCGGT 15
Db 3 CTCTTCGCGGT 13

```

```

RESULT 5
US-10-098-263B-110352
; Sequence 110352, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110352
Query Match 55.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCGC 11
Db 4 CCAACTCTTCGC 14

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RESULT 6

US-10-098-263B-129624
; Sequence 129624, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129624

Query Match 55.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1 CCAACTCTTCG 11
|||||
DB 9 CCAACTCTTCG 19

RESULT 7

US-08-961-888-12
; Sequence 12, Application US/08961888
; Patent No. US20010016351A1
; GENERAL INFORMATION:

; APPLICANT: Padgett, Kerstien
; TITLE OF INVENTION: Sorage, Joseph
; TITLE OF INVENTION: No. US20010016351A1 Vector For Gene Expression
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,888
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I
; REGISTRATION NUMBER: 32,660
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-7451
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
US-08-961-888-12

Query Match 55.0%; Score 11; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 5 CTCCTCGCGGT 15
|||||
DB 11 CTCCTCGCGGT 21

RESULT 8

US-10-002-050-29
; Sequence 29, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Semaphorins

; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically synthesized

US-10-002-050-29

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 10 CGCGGTGCAG 20
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DB 20 CGCGGTGCAG 30

RESULT 9

US-10-002-304-29
; Sequence 29, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby

; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002,304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

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; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-10-002-304-29

Query Match          55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
    |||||
Db 20 CGCGGTGGCAG 30

RESULT 10
US-10-003-152-29
; Sequence 29, Application US/10003152
; Patent No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1 Amino Acid Sequences for Human Semaphorin-1
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003.152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-10-003-152-29

Query Match          55.0%; Score 11; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
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Db 20 CGCGGTGGCAG 30

RESULT 11
US-09-971-894-12/c
; Sequence 12, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kashi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerstein, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR PROKARYOTE CLASSIFICAT
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
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; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-971-894-12

Query Match          50.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGCGGT 15
    |||||
Db 11 TCTTCGCGGT 2

RESULT 12
US-09-909-849-17
; Sequence 17, Application US/09909849
; Patent No. US20020106754A1
; GENERAL INFORMATION:
; APPLICANT: Tauch, Andreas
; TITLE OF INVENTION: Nucleotide Sequences Which Code for the alr Gene
; FILE REFERENCE: 032301 WD 173
; CURRENT APPLICATION NUMBER: US/09/909,849
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; OTHER INFORMATION:
US-09-909-849-17

Query Match          50.0%; Score 10; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCGGTGGCAG 20
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Db 11 GCGGTGGCAG 20

RESULT 13
US-09-853-526-420
; Sequence 420, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 420
; LENGTH: 21
; TYPE: DNA
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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer for SEQ 257, SEQ 334
US-09-853-526-420

Query Match      50.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCAACTCTTC 10
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Db       12 CCAACTCTTC 21

RESULT 14
US-09-901-484A-420
; Sequence 420, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T111XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
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; SEQ ID NO 420
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: downstream amplification primer for SEQ 257, SEQ 334
US-09-901-484A-420

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Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCAACTCTTC 10
        |||||
Db       12 CCAACTCTTC 21

RESULT 15
US-09-487-318-11/c
; Sequence 11, Application US/09487318
; Publication No. US20020182188A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Lola M
; APPLICANT: Nicholas, Moss
; APPLICANT: Hiroshi, Kubota
; TITLE OF INVENTION: Human Liver Progenitors
; FILE REFERENCE: 212875-00101
; CURRENT APPLICATION NUMBER: US/09/487,318
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/116,331
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; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-487-318-11

Query Match      50.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       22 CCAACTCTTCG 13

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGCGGTGGCAG 20

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Gapop 60.0 , Gapext 60.0

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3	20	100.0	30	1	PCT-US97-23619-5 Sequence 5, Appli
4	20	100.0	30	11	US-08-770-564A-5 Sequence 5, Appli
C 5	18	90.0	25	36	US-09-956-604-105231 Sequence 105231,
C 6	18	90.0	25	36	US-09-956-604A-105231 Sequence 105231,
C 7	18	90.0	25	36	US-09-956-604B-105231 Sequence 105231,
C 8	18	90.0	25	67	US-08-234-049-86453 Sequence 86453, A
C 9	16	80.0	24	9	US-08-521-634-15 Sequence 15, Appli
10	13	65.0	46	3	US-07-941-648-7 Sequence 7, Appli
11	13	65.0	46	8	US-08-441-893A-5 Sequence 5, Appli
12	13	65.0	46	16	US-09-253-006A-5 Sequence 5, Appli
13	13	65.0	46	18	US-09-461-908-5 Sequence 5, Appli
14	13	65.0	46	41	US-10-193-209-5 Sequence 5, Appli
15	12	60.0	21	1	PCT-US02-25940-14041 Sequence 14041, A
16	12	60.0	21	42	US-10-227-563-14041 Sequence 14041, A
C 17	12	60.0	25	26	US-09-660-220-6083 Sequence 6083, Ap
C 18	12	60.0	25	26	US-09-660-220-112404 Sequence 112404,
C 19	12	60.0	25	26	US-09-660-220-112414 Sequence 112414,
C 20	12	60.0	25	36	US-09-956-584-235506 Sequence 235506,
C 21	12	60.0	25	36	US-09-956-584-235507 Sequence 235507,

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22 12 60.0 25 67 US-60-232-638-71218
23 12 60.0 25 67 US-60-233-620-2716
24 12 60.0 25 67 US-60-233-620-80128
25 12 60.0 25 67 US-60-234-017-248486
26 12 60.0 25 67 US-60-234-017-248492
27 12 60.0 25 67 US-60-353-987-164100
28 12 60.0 25 67 US-60-353-987-205836
29 12 60.0 25 67 US-60-353-987-230113
30 12 60.0 25 67 US-60-353-987-244953
31 12 60.0 25 67 US-60-353-987-438619
32 12 60.0 25 67 US-60-353-987-615469
33 12 60.0 25 67 US-60-353-987-625356
34 12 60.0 25 67 US-60-353-987-654361
35 12 60.0 26 39 US-10-088-744-13
36 12 60.0 36 1 PCT-US02-25940-14042
37 12 60.0 36 42 US-10-227-563-14042
38 12 60.0 41 18 US-09-404-520-35075
39 11 55.0 18 28 US-09-703-708-11591
40 11 55.0 18 60 US-60-164-320-11591
41 11 55.0 18 62 US-60-183-791-11591
42 11 55.0 20 3 US-07-623-729A-13
43 11 55.0 20 3 US-07-748-564A-64
44 11 55.0 20 8 US-08-473-020-13
45 11 55.0 20 33 US-09-861-159-14

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ALIGNMENTS

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RESULT 1
PCT-US97-23619-7
; Sequence 7, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 16bc"
PCT-US97-23619-7
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCGCGGTGGCAG 20
Db 1 CCAACTCTTCGCGGTGGCAG 20
RESULT 2
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-7
Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCGCGGTGGCAG 20
Db 1 CCAACTCTTCGCGGTGGCAG 20
RESULT 3
PCT-US97-23619-5

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; Sequence 5, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "oligo 16"
PCT-US97-23619-5

Query Match .100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGTGGCAG 20
Db 11 CCAACTCTTCGCGTGGCAG 30

RESULT 4
US-08-770-564A-5
; Sequence 5, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-5

Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGTGGCAG 20
Db 11 CCAACTCTTCGCGTGGCAG 30

RESULT 5
US-09-956-604-105231/c
; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-105231

Query Match 90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGTGGCA 19
Db 21 CCAACTCTTCGCGTGGCA 4

RESULT 6
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
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; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
        |||||
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 7
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231

Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
        |||||
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 8
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          90.0%; Score 18; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
        |||||
Db      21 CAACTCTTCGCGGTGGCA 4

Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
        |||||
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 9
US-08-521-634-15/c
; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match          80.0%; Score 16; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCAACTCTTCGCGGTG 16
        |||||
Db      16 CCAACTCTTCGCGGTG 1

RESULT 10
US-07-941-648-7

Query Match          90.0%; Score 18; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
        |||||
Db      21 CAACTCTTCGCGGTGGCA 4
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; Sequence 7, Application US/07941648
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRL, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,648
; FILING DATE: 19920908
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
; US-07-941-648-7

Query Match 65.0%; Score 13; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
|||
Db 25 AACTCTTCGCGGT 37

RESULT 11
US-08-441-893A-5
; Sequence 5, Application US/08441893A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh 7200/90

; OPERATING SYSTEM: System 7.6
; SOFTWARE: Microsoft Word of Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,893A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; US-08-441-893A-5

Query Match 65.0%; Score 13; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
|||
Db 25 AACTCTTCGCGGT 37

RESULT 12
US-09-252-006A-5
; Sequence 5, Application US/09252006A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,006A
FILING DATE: 16-FEBRUARY-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/441,893
FILING DATE: 16-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 05-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,415
FILING DATE: 16-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/091,519
FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,211
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2003-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-09-252-006A-5

Query Match 65.0%; Score 13; DB 16; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37
|||||

RESULT 13
US-09-461-908-5
Sequence 5, Application US/09461908
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/199,209
FILING DATE: 19-Jul-2002

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,908
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/091,519
FILING DATE:
APPLICATION NUMBER: US/07/701,415
FILING DATE:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 06-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-09-461-908-5

Query Match 65.0%; Score 13; DB 18; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37
|||||

RESULT 14
US-10-199-209-5
Sequence 5, Application US/10199209
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/199,209
FILING DATE: 19-Jul-2002

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-10-199-209-5

Query Match 65.0%; Score 13; DB 41; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

RESULT 15
PCT-US02-25940-14041
; Sequence 14041, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14041
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1691485)...(1691505)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 16380
PCT-US02-25940-14041

Query Match 60.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCCGGGTGGC 18
Db 9 CTTCCGGGTGGC 20

Search completed: June 23, 2003, 16:08:20
Job time : 1678.53 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
Sequence: 1 CCAACTCTTCGCGTGGCAG 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
- 11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	80.0	21	1	PCT-US03-04088-588
C 2	16	80.0	23	1	PCT-US03-04088-530
C 3	14	70.0	19	1	PCT-US03-04088-258
C 4	14	70.0	21	1	PCT-US03-04088-593
C 5	14	70.0	25	12	US-60-427-836-401411
C 6	13	65.0	19	1	PCT-US03-04088-22
C 7	13	65.0	19	1	PCT-US03-04088-286
C 8	13	65.0	46	10	US-10-199-209A-5
C 9	12	60.0	23	1	PCT-US03-04088-522
C 10	12	60.0	23	1	US-10-367-892-14041
C 11	12	60.0	25	6	US-09-660-222-6083
C 12	12	60.0	25	6	US-09-660-222-112404
C 13	12	60.0	25	6	US-09-660-222-112414
C 14	12	60.0	25	7	US-09-953-570-71217
C 15	12	60.0	25	7	US-09-954-445A-2716
C 16	12	60.0	25	7	US-09-954-445A-80128
C 17	12	60.0	25	9	US-10-098-263B-31566
C 18	12	60.0	25	9	US-10-355-577-164100
C 19	12	60.0	25	9	US-10-355-577-205836
C 20	12	60.0	25	9	US-10-355-577-230113

C 21	12	60.0	25	9	US-10-355-577-244953	Sequence 244953,
C 22	12	60.0	25	9	US-10-355-577-438619	Sequence 438619, Ap
C 23	12	60.0	25	9	US-10-355-577-615469	Sequence 615469,
C 24	12	60.0	25	9	US-10-355-577-625356	Sequence 625356,
C 25	12	60.0	25	9	US-10-355-577-654361	Sequence 654361,
C 26	12	60.0	25	12	US-60-427-808-942586	Sequence 942586,
C 27	12	60.0	25	12	US-60-427-836-250708	Sequence 250708,
C 28	12	60.0	25	12	US-60-427-836-250709	Sequence 250709,
C 29	12	60.0	25	12	US-60-427-836-582453	Sequence 582453,
C 30	12	60.0	25	12	US-60-427-836-648877	Sequence 648877,
C 31	12	60.0	36	10	US-10-367-892-14042	Sequence 14042, A
C 32	11	55.0	15	10	US-10-299-054A-6945	Sequence 6945, Ap
C 33	11	55.0	15	10	US-10-299-054A-8164	Sequence 8164, Ap
C 34	11	55.0	17	10	US-10-299-054A-8610	Sequence 8610, Ap
C 35	11	55.0	17	10	US-10-299-054A-8620	Sequence 8620, Ap
C 36	11	55.0	22	9	US-10-310-188-70539	Sequence 70539, A
C 37	11	55.0	22	10	US-10-418-401-37	Sequence 37, Appl
C 38	11	55.0	24	9	US-10-310-188-7604	Sequence 7604, Ap
C 39	11	55.0	24	9	US-10-310-188-44232	Sequence 44232, A
C 40	11	55.0	25	7	US-09-953-570-48753	Sequence 48753, A
C 41	11	55.0	25	7	US-09-953-570-48758	Sequence 48758, A
C 42	11	55.0	25	7	US-09-953-570-126899	Sequence 126899,
C 43	11	55.0	25	7	US-09-953-570-126906	Sequence 126906,
C 44	11	55.0	25	7	US-09-953-570-129922	Sequence 129922,
C 45	11	55.0	25	7	US-09-953-570-134925	Sequence 134925,

ALIGNMENTS

RESULT 1

PCT-US03-04088-588/c
; Sequence 588, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 588
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-588

Query Match 80.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGGGTGGCAG 20
 Db 21 CTCTTCGGGTGGCAG 6

RESULT 2
 PCT-US03-04088-530/c
 ; Sequence 530, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 530
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-530

Query Match 80.0%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 5 CTCTTCGGGTGGCAG 20
 Db 23 CTCTTCGGGTGGCAG 8

RESULT 3
 PCT-US03-04088-258/c
 ; Sequence 258, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 258
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-258

Query Match 70.0%; Score 14; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCGGGTGGCAG 20
 Db 19 CTTCGGGTGGCAG 6

RESULT 4
 PCT-US03-04088-593
 ; Sequence 593, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 593
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
 ; OTHER INFORMATION: antisense region
 PCT-US03-04088-593

Query Match 70.0%; Score 14; DB 1; Length 21;
 Best Local Similarity 78.6%; Pred. No. 1.4e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCGGGTGGCAG 20
 Db 19 CTTCGGGTGGCAG 6

Db 1 CUUCGGGTGGCAG 14

RESULT 5
US-60-427-836-401411
; Sequence 401411, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 401411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-401411

Query Match 70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGGGTGGCA 19
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Db 4 TCTTCGGGTGGCA 17
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RESULT 6
PCT-US03-04088-22/c
; Sequence 22, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-22

Query Match 65.0%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCCGGGTGGCAG 20
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Db 1 UUCGGGTGGCAG 13
|||||

RESULT 8
US-10-199-209A-5
; Sequence 5, Application US/10199209A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Db 19 TTCGGGTGGCAG 7
|||||

RESULT 7
PCT-US03-04088-286
; Sequence 286, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-286

Query Match 65.0%; Score 13; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 5.6e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCGGGTGGCAG 20
|||||

Db 1 UUCGGGTGGCAG 13
|||||

RESULT 8
US-10-199-209A-5
; Sequence 5, Application US/10199209A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209A
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209A-5-

Query Match 65.0%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

RESULT 9
US-10-367-892-14041
; SEQUENCE 14041, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14041
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1691485)...(1691505)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 16380
US-10-367-892-14041

Query Match 60.0%; Score 12; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCCGGTGGC 18
Db 7 CTTCCGGTGGC 18

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Db 9 CTTCCGGTGGC 20

RESULT 10
PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 60.0%; Score 12; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGC 12
Db 12 CCAACTCTTCGC 1

RESULT 11
US-09-660-222-6083/c
; Sequence 6083, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6083
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D25217
US-09-660-222-6083

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Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGCGGTTGCA 19
| | | | | | | | | |
Db 17 TTGCGGTTGCA 6

RESULT 12
US-09-660-222-112404/c
; Sequence 112404, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X06617
US-09-660-222-112404

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTG 16
| | | | | | | | | |
Db 22 CTCTTCGCGGTG 11

RESULT 13
US-09-660-222-112414/c
; Sequence 112414, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112414
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X06617
US-09-660-222-112414

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTG 16
| | | | | | | | | |
Db 16 CTCTTCGCGGTG 5

RESULT 14
US-09-953-570-71217

; Sequence 71217, Application US/09953570
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71217
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-71217

Query Match 60.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCTTCGCGGTG 17
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Db 3 TCTTCGCGGTG 14

RESULT 15
US-09-954-445A-2716
; Sequence 2716, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2716
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-2716

Query Match 60.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACTCTTCGCGGT 15
| | | | | | | | | |
Db 13 ACTCTTCGCGGT 24

Search completed: June 23, 2003, 19:12:11
Job time : 877.928 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGGCAG 20

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	55.0	12	13	BM398341
2	11	55.0	19	13	BM401213
3	11	55.0	20	13	BM395007
4	11	55.0	26	13	BM399150
5	11	55.0	33	13	BM398611
6	11	55.0	34	17	AL759526 Arabidops

c

ALIGNMENTS

RESULT 1
BM398341
LOCUS
DEFINITION
5009-0-44-D05.t.2 Chilcoat/Turkewitz CDNA (large fraction)
Tetrahymena thermophila CDNA, mRNA sequence.
ACCESSION
BM398341
VERSION
BM398341.1 GI:18198394
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobucher, L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..12
/organism="Tetrahymena thermophila"
/strain="CU428.1"

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/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      1 a      4 c      6 g      1 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
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Db      2 CGCGGTGGCAG 12

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LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION      5009-0-84-C02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM401213
VERSION      BM401213.1 GI:18201266
KEYWORDS
SOURCE      Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713.

TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..20
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      3 a      5 c      8 g      3 t
ORIGIN
Query Match      55.0%; Score 11; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
      |||||
Db      9 CGCGGTGGCAG 19

RESULT 3
BM395007
LOCUS      20 bp mRNA linear EST 17-JAN-2002
DEFINITION      50072-2-7-A08.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395007
VERSION      BM395007.1 GI:18195060
KEYWORDS
SOURCE      Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713.

TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..19
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/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      3 a      5 c      8 g      3 t
ORIGIN
Query Match      55.0%; Score 11; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
      |||||
Db      9 CGCGGTGGCAG 19

RESULT 4
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Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399150
VERSION      BM399150.1 GI:18199203
KEYWORDS
SOURCE      Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713.

TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..26
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/strain="CU428.1"
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      8 a      5 c      10 g      3 t
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713.

TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
      |||||
Db      5 CGCGGTGGCAG 15

RESULT 4
BM399150
LOCUS      26 bp mRNA linear EST 17-JAN-2002
DEFINITION      5009-0-54-All.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399150
VERSION      BM399150.1 GI:18199203
KEYWORDS
SOURCE      Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713.

TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      8 a      5 c      10 g      3 t
ORIGIN

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Query Match 55.0%; Score 11; DB 13; Length 26;
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
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 Db 16 CGCGGTGGCAG 26

RESULT 5
 BM398611
 LOCUS
 DEFINITION 5009-0-47-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398611
 VERSION BM398611.1 GI:18198664
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E., Frankel
 J. and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 J. and Klobutcher, L.
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
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 1..33 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /notes="Vector: Bluescript 2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 5 a 10 c 12 g 6 t

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 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
 |||||
 Db 9 CGCGGTGGCAG 19

RESULT 6
 AL759526/c
 LOCUS
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-188A07-014624,
 genomic survey sequence.
 ACCESSION AL759526
 VERSION AL759526.1 GI:21497874
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
 and Weisshaar, B.
 TITLE A pipeline for automated high-throughput generation of PSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

transformed lines
 Unpublished
 2
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 34)
 Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene Atlg9790. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/
 Location/Qualifiers
 1..34
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 10 a 9 c 9 g 6 t

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
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Qy 6 TCTTCGCGGTG 16
 |||||
 Db 13 TCTTCGCGGTG 3

RESULT 7
 BJ063841
 LOCUS
 DEFINITION laevis cDNA clone XLO77114 5', mRNA sequence.
 ACCESSION BJ063841
 VERSION BJ063841.1 GI:17471031
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers

```

source
1. 37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL077114"
/library="NIBB Mochii normalized Xenopus tailbud"
/tissue="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; CDNAS
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT      5 a 15 c 3 g 13 t 1 others
ORIGIN

Query Match      55.0%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11
Db 24 CCAACTCTTCG 34

RESULT 8
LOCUS BH851915/c
DEFINITION SALK_073707.54.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_073707.54.25.x, DNA
sequence.
ACCESSION BH851915
VERSION BH851915.1 GI:21422786
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 40)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g46110.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1. 40
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_073707.54.25.x"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      7 a 11 c 12 g 10 t
ORIGIN

Query Match      55.0%; Score 11; DB 17; Length 40;

```

```

Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTCGCGGTGGC 18
Db 27 TTCGCGGTGGC 17

RESULT 9
LOCUS BM400948
DEFINITION 5009-0-80-E05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400948
VERSION BM400948.1 GI:18201001
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 44)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Kloubutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1. 44
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      10 a 11 c 14 g 8 t 1 others
ORIGIN

Query Match      55.0%; Score 11; DB 13; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
Db 15 CGCGGTGGCAG 25

RESULT 10
LOCUS BM397151
DEFINITION 5009-0-29-F01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397151
VERSION BM397151.1 GI:18197204
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 45)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Kloubutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Molecular Genetics and Cell Biology

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University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES

source

Location/Qualifiers

1. .45
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

10 a 11 c 15 g

ORIGIN

Query Match

55.0%; Score 11; DB 13; Length 45;

Best Local Similarity

100.0%; Pred. No. 1.6e+04;

Matches 11; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGTGGCAG 20

Db 16 CGCGTGGCAG 26

RESULT 11

AA813480

LOCUS

DEFINITION

aa167a09.s1 Soares testis NHT Homo sapiens cDNA clone 1375864 3', similar to SW:CAV3_MOUSE P51637 CAVEOLIN-3 ; mRNA sequence.

ACCESSION

AA813480

VERSION

AA813480.1 GI:2882165

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 49)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-i@mail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 1418 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="1375864"

/clone_lib="Soares_testis_NHT"

/sex="male"

/lab host="DH10B"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, inc., and primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAATGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT

7 a 21 c 11 g 10 t

ORIGIN

Query Match

55.0%; Score 11; DB 9; Length 49;

Best Local Similarity

100.0%; Pred. No. 1.6e+04;

Matches 11; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACTCTCGCGG 14

Db 28 ACTCTCGCGG 38

RESULT 12

AU106839

LOCUS

DEFINITION

AU106839 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

KAT08593, mRNA sequence.

ACCESSION

AU106839

VERSION

AU106839.1 GI:13556360

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki, T., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata

, H., Oca, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki

, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

21270072

COMMENT

Contact: Yutaka Suzuki

Department of Medical Science, University of Tokyo

Institute of Medical Science, Minatoku, Tokyo 108-8639, Japan

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, T., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

, S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="KAT08593"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT

13 a 14 c 17 g 6 t

ORIGIN

Query Match

55.0%; Score 11; DB 9; Length 50;

Best Local Similarity

100.0%; Pred. No. 1.6e+04;

Matches 11; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11

Db 29 CCAACTCTTCG 39

RESULT 13

BM396493

LOCUS

DEFINITION

BM396493 5009-0-21-B08.t.2 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM396493

VERSION

BM396493.1 GI:18196516

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila.

14 bp mRNA linear EST 17-JAN-2002

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 14)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

Location/Qualifiers

1..14

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

3 a 5 c 5 g 1 t

BASE COUNT

ORIGIN

Query Match 50.0%; Score 10; DB 13; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.1e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 5 CGCGGTGGCA 14

RESULT 14

LOCUS

BM396941 17 bp mRNA linear EST 17-JAN-2002

5009-0-27-B04.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

BM396941

ACCESSION BM396941.1 GI:18196994

KEYWORDS EST.

SOURCE Tetrahymena thermophila.

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

Location/Qualifiers

1..17

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match 50.0%; Score 10; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 5 CGCGGTGGCA 14

RESULT 15

LOCUS

BM675715/c

DEFINITION

BM675715

ACCESSION

BM675715.1

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Sus scrofa

pig.

Eukaryota;

Mammalia;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

Mammalia;

Eutheria;

Cetartiodactyla;

Suina;

Suidae;

Sus.

1 (bases 1 to 18)

AUTHORS

Adelson, D.L. and Gill, C.A.

TITLE

Porcine ESTs

JOURNAL

Unpublished (2002)

COMMENT

Contact: David L. Adelson

Animal Breeding and Genetics

Texas A&M University

Animal Science Dept., TAMU-2471,

College Station, TX 77843-2471,

USA

Tel: 9798452616

Fax: 9798456970

Email: david.adelson@tamu.edu.

Location/Qualifiers

1..18

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="CSEQFL35 adipose"

/tissue_type="adipose tissue"

/note="Organ: adipose tissue;

Vector: pBluescript SK+;

Site 1: NotI; Site 2: EcoRI;

sequence 5' of the insert

(5'-NNN...NNNinsert)

CGCAATTGGAGCTCCACCGGTGGCGCGGCTCGAG. Sequence 3' of

the inserts (AAGATTCGATATCAAGCTTATCGATACCGTCCGCTCGAG.

non-normalized library, sequenced 3' with M13R primer."

2 a 6 c 7 g 3 t

BASE COUNT

ORIGIN

Query Match 50.0%; Score 10; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 10 CGCGGTGGCA 1

Search completed: June 23, 2003, 10:10:22

Job time : 1032.31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20

Sequence: 1 CCAACTCTTCGCGGTGCAG 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	30	2	US-08-770-565-7
2	20	100.0	30	2	US-08-770-565-5
3	14	70.0	45	6	5198342-4
4	13.6	68.0	49	4	US-09-166-9665-3
5	13.4	67.0	46	1	US-08-091-519-5
6	13.4	67.0	46	1	US-08-106-507-7
7	13.4	67.0	46	1	US-08-442-043A-5
8	13.4	67.0	46	5	PCT-US91-03478-5
9	13.2	66.0	36	3	US-08-833-167-69
10	13.2	66.0	36	4	US-09-344-837A-69
11	12.8	64.0	22	1	US-08-599-252-36
12	12.8	64.0	22	5	PCT-US96-06352-36
13	12.8	64.0	22	5	PCT-US96-06583-36
14	12.8	64.0	27	1	US-07-807-529A-64
15	12.6	63.0	28	4	US-08-948-381-3
16	12.6	63.0	30	1	US-08-181-556-9
17	12.4	62.0	20	3	US-09-235-246-14
18	12.4	62.0	38	1	US-08-664-449-61
19	12.4	62.0	47	4	US-09-641-638-1257
20	12.2	61.0	21	4	US-07-974-409C-41
21	12.2	61.0	21	4	US-07-974-409C-48
22	12.2	61.0	21	4	US-07-974-409C-48
23	12.2	61.0	36	1	US-08-136-742A-4
24	12.2	61.0	36	3	US-09-248-026-4
25	12.2	61.0	36	5	PCT-US93-11667-4
26	12.2	61.0	37	3	US-08-318-794-12
27	12.2	61.0	37	4	US-08-470-106-12

28	12.2	61.0	41	1	US-08-110-294A-27	Sequence 27, Appl
29	12.2	61.0	41	2	US-08-389-926-27	Sequence 27, Appl
30	12	60.0	25	1	US-08-623-891-81	Sequence 81, Appl
31	12	60.0	25	4	US-09-340-861-81	Sequence 81, Appl
32	12	60.0	25	4	US-09-634-262-81	Sequence 81, Appl
33	11.8	59.0	21	4	US-09-536-936-3	Sequence 3, Appl
34	11.8	59.0	22	4	US-09-240-918-65	Sequence 65, Appl
35	11.8	59.0	25	1	US-08-977-818-16	Sequence 16, Appl
36	11.8	59.0	25	2	US-08-670-274B-16	Sequence 16, Appl
37	11.8	59.0	25	4	US-09-146-187-16	Sequence 16, Appl
38	11.8	59.0	44	1	US-08-530-492-52	Sequence 52, Appl
39	11.8	59.0	44	4	US-08-906-517-52	Sequence 52, Appl
40	11.8	59.0	45	2	US-08-632-882-5	Sequence 5, Appl
41	11.8	59.0	46	1	US-08-741-881-39	Sequence 39, Appl
42	11.8	59.0	46	1	US-08-739-158-39	Sequence 39, Appl
43	11.8	59.0	46	2	US-08-739-167-39	Sequence 39, Appl
44	11.8	59.0	46	3	US-08-404-796-39	Sequence 39, Appl
45	11.8	59.0	46	3	US-08-931-869-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 CCAACTCTTCGCGGTGCAG 20

```
Db      1 CCAACTCTTCGGGTGGCAG 20
|||||
RESULT 2
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; FILE REFERENCE: 32350-150960
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5
Query Match      100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCAACTCTTCGGGTGGCAG 20
Db      11 CCAACTCTTCGGGTGGCAG 30
|||||
RESULT 3
5198342-4
; Patent No. 5198342
; APPLICANT: MALIISZEWSKI, CHARLES R.
; TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/548,059
; FILING DATE: 03-JUL-1990
; SEQ ID NO: 4:
; LENGTH: 45
5198342-4
Query Match      70.0%; Score 14; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCAACTCTTCGGGT 15
|||||
Db      23 CCAACTCTTCGGGT 36
|||||
RESULT 4
US-09-166-966E-3/c
; Sequence 3, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-166-966E-3
Query Match      68.0%; Score 13.6; DB 4; Length 49;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CCAACTCTTCGGGTGGCAG 20
Db      30 CCAACTGGTCGGGTGACAG 11
|||||
RESULT 5
US-08-091-519-5
; Sequence 5, Application US/08091519
; Patent No. 5350683
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/573,576
;; FILING DATE: 24-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/627,071
;; FILING DATE: 13-DEC-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wight, Christopher L.
;; REGISTRATION NUMBER: 31680
;; REFERENCE/DOCKET NUMBER: 2003-C
;; TELEPHONE: 206-587-5570
;; TELEFAX: 206-233-0644
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
US-08-091-519-5

Query Match 67.0%; Score 13.4; DB 1; Length 46;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGT 15
| | | | | | | | | | | | | | | | | |
DB 23 CAAACTCTTCGCGGT 37

RESULT 6
US-08-106-507-7
; Sequence 7, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE:
;; CLONE: oligonucleotide
US-08-106-507-7

Query Match 67.0%; Score 13.4; DB 1; Length 46;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGT 15
| | | | | | | | | | | | | | | | | |
DB 23 CAAACTCTTCGCGGT 37

RESULT 7
US-08-442-043A-5
; Sequence 5, Application US/08442043A
; Patent No. 5767064
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,043A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

Best Local Similarity 93.3%; Pred. No. 4e+02; Length 46;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 CCAACTCTTCGGCGT 15
Db 23 CAAACTCTTCGGCGT 37

RESULT 9
US-08-833-167-69
; Sequence 69, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA (synthetic)"
; US-08-833-167-69

Query Match 66.0%; Score 13.2; DB 3; Length 36;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGCGTGC 18
Db 19 CCAGCTCTTCGGCGTGC 36

RESULT 10
US-09-344-837A-69
; Sequence 69, Application US/09344837A

LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-442-043A-5

Query Match 67.0%; Score 13.4; DB 1; Length 46;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 CCAACTCTTCGGCGT 15
Db 23 CAAACTCTTCGGCGT 37

RESULT 8
PCT-US91-03478-5
; Sequence 5, Application PC/TUS9103478
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03478
; FILING DATE: 19910517
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
PCT-US91-03478-5

Query Match 67.0%; Score 13.4; DB 5; Length 46;


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; Patent No. 6358505
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. CHRISTOPHER BAUER
; ADDRESSEE: MONSANTO/G. D. SEARLE & CO.,
; ADDRESSEE: PATENT DEPARTMENT CENTRAL
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344, 837A
; FILING DATE: 25-JUN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. CHRISTOPHER BAUER
; REFERENCE/DOCKET NUMBER: 2907/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 636-737-6257
; TELEFAX: 636-737-5452
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA (synthetic)"
; US-09-344-837A-69

Query Match 66.0%; Score 13.2; DB 4; Length 36;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTTTCGCGGTGC 18
    ||| ||| ||| ||| |||
Db 19 CCAGCTCTCGGGTGC 36

RESULT 11
US-08-599-252-36
; Sequence 36, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIKKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06352
; FILING DATE:
; CLASSIFICATION:

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; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,252
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9053-0001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-599-252-36

Query Match 64.0%; Score 12.8; DB 1; Length 22;
Best Local Similarity 87.5%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACTCTTCGCGGTGGCA 19
    ||| ||| ||| ||| |||
Db 1 ACTCTTCGCGGTGGCA 16

RESULT 12
PCT-US96-06352-36
; Sequence 36, Application PC/TUS9606352
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIKKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06352
; FILING DATE:
; CLASSIFICATION:

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FILING DATE: 09-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 9053-0001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-06352-36

Query Match 64.0%; Score 12.8; DB 5; Length 22;
 Best Local Similarity 87.5%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCA 19
 Db 1 ACTCTTCGGGTGGCA 16

RESULT 13
 PCT-US96-06583-36
 Sequence 36, Application PC/TUS9606583
 GENERAL INFORMATION:
 APPLICANT: DRYNA, DENNIS T.
 APPLICANT: FEDER, JOHN N.
 APPLICANT: GNIRKE, ANDREAS
 APPLICANT: KIMMEL, BRUCE E.
 APPLICANT: THOMAS, WINSTON J.
 APPLICANT: WOLFE, ROGER K.
 TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
 TITLE OF INVENTION: HEMOCHROMATOSIS
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06583
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/599,252
 FILING DATE: 09-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 9053-0001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-06583-36

Query Match 64.0%; Score 12.8; DB 5; Length 22;
 Best Local Similarity 87.5%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCA 19
 Db 1 ACTCTTCGGGTGGCA 16

RESULT 14
 US-07-807-529A-64
 Sequence 64, Application US/07807529A
 Patent No. 5547669
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: One Kendall Square, Building 600
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02139
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/807,529A
 FILING DATE: 19911213
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Channing, Stacey L.
 REGISTRATION NUMBER: 31,095
 REFERENCE/DOCKET NUMBER: IPC-027/imi-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 494-0060
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-07-807-529A-64

Query Match 64.0%; Score 12.8; DB 1; Length 27;
 Best Local Similarity 87.5%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGTGGC 18
 Db 5 AATCTTCGGGTGGC 20

RESULT 15
 US-08-948-381-3
 Sequence 3, Application US/08948381
 Patent No. 6274341

```

; GENERAL INFORMATION:
; APPLICANT: Bailey, James E.
; APPLICANT: Fussenegger, Martin
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: A NOVEL CYTOSTATIC PROCESS
; TITLE OF INVENTION: INCREASES THE PRODUCTIVITY OF CULTURED CELLS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,381
; FILING DATE: 14-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 009187-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-948-381-3

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Query Match      63.0%; Score 12.6; DB 4; Length 28;
Best Local Similarity 79.9%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CCAACTCTTCGCGTGGA 19
Db      4 CGAATCTTCGCGGGA 22

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Search completed: June 25, 2003, 00:24:38
Job time : 31.3586 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGCAG 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	67.0	46	9	US-10-199-209-5
2	12.8	64.0	27	7	US-08-464-363-64
3	12.6	63.0	20	9	US-09-954-556-39
4	12.6	63.0	24	10	US-09-820-339A-23
5	12.4	62.0	25	9	US-10-098-263B-31566
6	12.2	61.0	20	10	US-09-909-849-17
7	12.2	61.0	21	9	US-09-943-388-21
8	12.2	61.0	21	9	US-10-002-974-50
9	12.2	61.0	21	12	US-10-014-269-50
10	12.2	61.0	23	9	US-10-084-826-37
11	12.2	61.0	23	10	US-09-844-508-37
12	12.2	61.0	25	9	US-10-098-263B-12812
13	12.2	61.0	36	9	US-09-568-756-4
14	12.0	60.0	23	9	US-09-961-001-6
15	12.0	60.0	25	9	US-10-098-263B-46129
16	12.0	60.0	25	9	US-10-098-263B-100241
17	12.0	60.0	25	9	US-10-098-263B-116734
18	12.0	60.0	33	9	US-09-416-579A-11
19	11.8	59.0	25	9	US-10-098-263B-47805

ALIGNMENTS

RESULT 1
US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US2003006016A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; Cosman, David J.
; Lupton, Stephen D.
; Mosley, Bruce A.
; Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:

Sequence 54377, A
Sequence 65405, A
Sequence 65406, A
Sequence 84572, A
Sequence 87104, A
Sequence 115897, A
Sequence 125149, A
Sequence 16, Appli
Sequence 9, Appli
Sequence 1234, Ap
Sequence 5, Appli
Sequence 116, App
Sequence 12433, A
Sequence 30410, A
Sequence 31554, A
Sequence 61048, A
Sequence 121314, A
Sequence 124383, A
Sequence 2279, Ap
Sequence 2528, Ap
Sequence 4623, Ap
Sequence 4831, Ap
Sequence 1061, Ap
Sequence 1134, Ap
Sequence 1303, Ap
Sequence 1362, Ap

20 11.8 59.0 25 9 US-10-098-263B-54377
21 11.8 59.0 25 9 US-10-098-263B-65405
22 11.8 59.0 25 9 US-10-098-263B-65406
23 11.8 59.0 25 9 US-10-098-263B-84572
24 11.8 59.0 25 9 US-10-098-263B-87104
25 11.8 59.0 25 9 US-10-098-263B-115897
26 11.8 59.0 25 9 US-10-098-263B-125149
27 11.8 59.0 25 10 US-09-804-690-16
28 11.8 59.0 49 9 US-10-103-480-9
29 11.8 59.0 49 9 US-09-961-077-1234
30 11.8 59.0 49 10 US-09-812-186-5
31 11.6 58.0 24 9 US-09-940-185-116
32 11.6 58.0 25 9 US-10-098-263B-12433
33 11.6 58.0 25 9 US-10-098-263B-30410
34 11.6 58.0 25 9 US-10-098-263B-31554
35 11.6 58.0 25 9 US-10-098-263B-61048
36 11.6 58.0 25 9 US-10-098-263B-121314
37 11.6 58.0 25 9 US-10-098-263B-124383
38 11.6 58.0 31 9 US-09-864-785-2279
39 11.6 58.0 31 9 US-09-864-785-2528
40 11.6 58.0 31 9 US-09-877-478-4623
41 11.6 58.0 31 9 US-09-877-478-4831
42 11.6 58.0 31 9 US-10-163-552-1061
43 11.6 58.0 31 9 US-10-163-552-1134
44 11.6 58.0 31 9 US-10-163-552-1303
45 11.6 58.0 31 9 US-10-163-552-1362

NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5

Query Match 67.0%; Score 13.4; DB 9; Length 46;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGCGT 15
| | | | | | | | | | | | | | | | | | | | |
Db 23 CAAACTCTTCGGCGT 37

RESULT 2
US-08-464-363-64
; Sequence 64, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBINOPEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-464-363-64

Query Match 64.0%; Score 12.8; DB 7; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTCTTCGGCGTGC 18
| | | | | | | | | | | | | | | | | | | | |
Db 5 AATCTTTGCGGTGC 20

RESULT 3
US-09-954-556-39
; Sequence 39, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-39

Query Match 63.0%; Score 12.6; DB 9; Length 20;
Best Local Similarity 78.9%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGCGTGGCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 2 CCAACTGATCAGCGCGCA 20

RESULT 4
US-09-820-339A-23/c
; Sequence 23, Application US/09820339A
; Patent No. US20020081652A1
; GENERAL INFORMATION:
; APPLICANT: FUCHS, Sara
; APPLICANT: BARCHAN, Dora
; APPLICANT: SOUROUJON, Miriam
; TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND THE
; TITLE OF INVENTION: FOR TREATMENT OF MYASTHENIA GRAVIS
; FILE REFERENCE: FUCHS-2A
; CURRENT APPLICATION NUMBER: US/09/820,339A
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 09/423,398
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: PCT/IL98/00211
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-820-339A-23

Query Match 63.0%; Score 12.6; DB 10; Length 24;
Best Local Similarity 78.9%; Pred. No. 3e+03;


```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-014-269-50

Query Match      61.0%; Score 12.2; DB 12; Length 21;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      1 AGTCTTCTGGGTGGCAG 17

RESULT 10
US-10-084-826-37/c
; Sequence 37, Application US/10084826
; Publication No. US20030049649A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan P.
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/10/084,826
; CURRENT FILING DATE: 2002-02-24
; PRIOR APPLICATION NUMBER: 09/844,508
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GAPDH probe
US-10-084-826-37

Query Match      61.0%; Score 12.2; DB 9; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      19 AGTCTTCTGGGTGGCAG 3

RESULT 11
US-09-844-508-37/c
; Sequence 37, Application US/09844508
; Patent No. US20020115215A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/09/844,508
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GAPDH probe
US-09-844-508-37

Query Match      61.0%; Score 12.2; DB 10; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      19 AGTCTTCTGGGTGGCAG 3

RESULT 12
US-10-098-263B-12812
; Sequence 12812, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-12812

Query Match      61.0%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      2 ACACGTCGCGGTGGAAG 18

RESULT 13
US-09-568-756-4/c
; Sequence 4, Application US/09568756
; Patent No. US20020164782A1
; GENERAL INFORMATION:
; APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith, A.E.
; TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE & RAYMOND
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,756
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,742
; FILING DATE: 13-OCT-1993
; APPLICATION NUMBER: US 07/985,478
; FILING DATE: 03-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A30668A

```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-014-269-50

Query Match      61.0%; Score 12.2; DB 12; Length 21;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      1 AGTCTTCTGGGTGGCAG 17

RESULT 10
US-10-084-826-37/c
; Sequence 37, Application US/10084826
; Publication No. US20030049649A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan P.
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/10/084,826
; CURRENT FILING DATE: 2002-02-24
; PRIOR APPLICATION NUMBER: 09/844,508
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GAPDH probe
US-10-084-826-37

Query Match      61.0%; Score 12.2; DB 9; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      19 AGTCTTCTGGGTGGCAG 3

RESULT 11
US-09-844-508-37/c
; Sequence 37, Application US/09844508
; Patent No. US20020115215A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/09/844,508
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GAPDH probe
US-09-844-508-37

Query Match      61.0%; Score 12.2; DB 10; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      19 AGTCTTCTGGGTGGCAG 3

RESULT 12
US-10-098-263B-12812
; Sequence 12812, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-12812

Query Match      61.0%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 ACTCTTCGCGGTGGCAG 20
      | | | | | | | | | |
Db      2 ACACGTCGCGGTGGAAG 18

RESULT 13
US-09-568-756-4/c
; Sequence 4, Application US/09568756
; Patent No. US20020164782A1
; GENERAL INFORMATION:
; APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith, A.E.
; TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE & RAYMOND
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,756
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,742
; FILING DATE: 13-OCT-1993
; APPLICATION NUMBER: US 07/985,478
; FILING DATE: 03-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A30668A

```


TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 408-2500
 TELEFAX: (212) 765-2519
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-568-756-4

Query Match 61.0%; Score 12.2; DB 9; Length 36;
 Best Local Similarity 82.4%; Pred. No. 4.8e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AACTCTTCGGGTGGCA 19
 |||||
 Db 26 AACTCTACTCGGTGGCA 10

RESULT 14
 US-09-961-001-6
 ; Sequence 6, Application US/09961001
 ; Publication No. US20030109466A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF KSR EXPRESSION
 ; FILE REFERENCE: RTS-0280
 ; CURRENT APPLICATION NUMBER: US/09/961,001
 ; CURRENT FILING DATE: 2001-09-20
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 6
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR Probe
 US-09-961-001-6

Query Match 60.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGGTGGCAG 20
 |||||
 Db 3 CCAAGTCTGCTGTCGCAG 22

RESULT 15
 US-10-098-263B-46129/c
 ; Sequence 46129, Application US/10098263B
 ; Publication No. US2003010410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 46129
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-46129

Query Match 60.0%; Score 12; DB 9; Length 25;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCAACTCTTCGGGTGGCAG 20
 |||||
 Db 25 CCAAGTCTTCGAGAGGGTAG 6

Search completed: June 25, 2003, 22:25:05
 Job time : 61.7968 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1697.05 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGCGGTGCAG 20

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	20	100.0	20	11	US-08-770-564A-7
3	20	100.0	30	1	PCT-US97-23619-5
4	20	100.0	30	11	US-08-770-564A-5
5	18	90.0	25	36	US-09-956-604-105231
6	18	90.0	25	36	US-09-956-604A-105231
7	18	90.0	25	36	US-09-956-604B-105231
8	18	90.0	25	67	US-60-234-049-86453
9	16	80.0	24	9	US-08-521-634-15
10	14.2	71.0	25	36	US-09-954-427-198291
11	14.2	71.0	25	36	US-09-956-584-564849
12	14.2	71.0	25	67	US-60-233-166-198291
13	14.2	71.0	25	67	US-60-234-017-550890
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15	14.2	71.0	36	17	US-09-338-248-42
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20	13.8	69.0	25	67	US-60-234-017-550884
21	13.8	69.0	25	79	US-60-353-987-283954
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C 26	13.6	68.0	25	36	US-09-956-584-392741
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C 28	13.6	68.0	25	36	US-09-956-604-67492
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C 32	13.6	68.0	25	67	US-60-234-017-294574
C 33	13.6	68.0	25	67	US-60-234-017-136320
C 34	13.6	68.0	25	67	US-60-234-017-446035
C 35	13.6	68.0	25	67	US-60-234-017-490416
C 36	13.6	68.0	25	67	US-60-234-049-92079
C 37	13.6	68.0	25	79	US-60-353-987-850409
C 38	13.6	68.0	41	18	US-09-404-520-28958
C 39	13.6	68.0	41	79	US-60-353-790-1064
C 40	13.6	68.0	50	29	US-09-755-374A-17486
C 41	13.6	68.0	50	29	US-09-755-374B-17488
C 42	13.4	67.0	25	17	US-09-336-196P-55504
C 43	13.4	67.0	25	17	US-09-336-196P-55515
C 44	13.4	67.0	25	17	US-09-336-196G-59504
C 45	13.4	67.0	25	17	US-09-336-196G-59515

ALIGNMENTS

RESULT 1
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 ; Sequence 7, Application PC/TUS9723619
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; TITLE OF INVENTION: "Methods for Detecting and Inhibiting the
 ; TITLE OF INVENTION: RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/23619
 ; FILING DATE: Not yet assigned
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,564
 ; FILING DATE: 20-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,565
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 15389-27PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 7:
 ; -SEQUENCE CHARACTERISTICS:

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; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 16bc"
PCT-US97-23619-7

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Best Local Similarity 100.0%; Pred.No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

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DB    1 CCAACTCTTCGGGTGGCAG 20

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US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T..
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-7

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5

; Sequence 5, Application PC/TUS9723619
; GENERAL INFORMATION:

; APPLICANT:

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; APPLICANT:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; RNA Component of Telomerase

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/23619

; FILING DATE: Not yet assigned

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/770,564

; FILING DATE: 20-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/770,565

; FILING DATE: 20-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 15389-27PC

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

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; NAME/KEY: -

; LOCATION: 1..30

; OTHER INFORMATION: /note= "oligo 16"

; PCT-US97-23619-5

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Best Local Similarity 100.0%; Pred. No. 8.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCAG 20

Db 11 CCAACTCTTCGCGGTGGCAG 30

RESULT 4

US-08-770-564A-5

; Sequence 5, Application US/08770564A

; GENERAL INFORMATION:

; APPLICANT: Kealey, James T.

; APPLICANT: Pruzan, Ron

; TITLE OF INVENTION: Inhibitory Polynucleotides Directed

; AGAINST THE RNA COMPONENT OF TELOMERASE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/770,564A

; FILING DATE: 20-DEC-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-002200US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-770-564A-5

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Best Local Similarity 100.0%; Pred. No. 8.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 CCAACTCTTCGCGGTGGCAG 30

RESULT 5

US-09-956-604-105231/c

; Sequence 105231, Application US/09956604

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

; FILE REFERENCE: 3117.1

; CURRENT APPLICATION NUMBER: US/09/956,604

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/234,049

; PRIOR FILING DATE: 2000-09-19

; NUMBER OF SEQ ID NOS: 141629

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 105231

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Escherichia coli

; US-09-956-604-105231

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Best Local Similarity 100.0%; Pred. No. 90;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGGTGGCA 19

Db 21 CCAACTCTTCGCGGTGGCA 4

RESULT 6

US-09-956-604A-105231/c

; Sequence 105231, Application US/09956604A

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

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; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; ORIGIN: 956-604A-105231

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Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 CAACTCTTCGCGGTGCA 19
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Db 21 CAACTCTTCGCGGTGCA 4

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RESULT 7
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; ORIGIN: 956-604B-105231

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Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 CAACTCTTCGCGGTGCA 19
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Db 21 CAACTCTTCGCGGTGCA 4

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RESULT 8
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

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Query Match          90.0%; Score 18; DB 67; Length 25;

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Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CAACTCTTCGCGGTGCA 4

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RESULT 9
US-08-521-634-15/c
; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

```

```

Query Match          80.0%; Score 16; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CCAACTCTTCGCGGTG 16
   |||||
Db 16 CCAACTCTTCGCGGTG 1

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```

RESULT 10
US-09-954-427-198291

```

; Sequence 198291, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-09-954-427-198291

Query Match 71.0%; Score 14.2; DB 36; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGGTGGCA 20
||| ||||| ||||| |||||
Db 7 CAAGACTTCGACGTGGCAG 25

RESULT 11
US-09-956-584-564849/c
; Sequence 564849, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mitmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 564849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-564849

Query Match 71.0%; Score 14.2; DB 36; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
Db 20 CCACCTCTCGCGGTGGTA 2

RESULT 12
US-60-233-166-198291
; Sequence 198291, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198291

Query Match 71.0%; Score 14.2; DB 67; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGGTGGCAG 20
||| ||||| ||||| |||||
Db 7 CAAGACTTCGACGTGGCAG 25

RESULT 13
US-60-234-017-550890/c
; Sequence 550890, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mitmann, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV100189
US-60-234-017-550890

Query Match 71.0%; Score 14.2; DB 67; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
Db 20 CCACCTCTCGCGGTGGTA 2

RESULT 14
US-60-353-987-207601/c
; Sequence 207601, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mitmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 207601
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-207601

Query Match 71.0%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
Db 21 CCACCTCTTCAGGGGGCA 3

RESULT 15
US-09-338-248-42/c
; Sequence 42, Application US/09338248
; GENERAL INFORMATION:

```

; APPLICANT: Lee, Stephen C
; TITLE OF INVENTION: Method of producing permutaseins by
; FILE OF INVENTION: Scanning permutagenesis
; FILE REFERENCE: C 3041
; CURRENT APPLICATION NUMBER: US/09/338,248
; CURRENT FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Synthetic
; US-09-338-248-42

```

```

Query Match      71.0%; Score 14.2; DB 17; Length 36;
Best Local Similarity 84.2%; Pred. No. 9e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

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Qy      1 CCAACTCTTGGCGGTGGCA 19
         |||||
Db      34 CCAGCTCCTCGGGTGGCA 16

```

Search completed: June 25, 2003, 06:20:25
Job time : 1698.67 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGGCAG 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US12_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US13_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US17_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	80.0	21	1	PCT-US03-04088-588
C 2	16	80.0	23	1	PCT-US03-04088-530
C 3	14.8	74.0	31	6	US-09-890-648-6
C 4	14.8	74.0	43	10	US-10-299-054A-7701
C 5	14.2	71.0	25	9	US-10-355-577-207601
C 6	14.2	71.0	25	12	US-60-427-808-776553
C 7	14.2	71.0	34	5	US-09-462-405C-4
C 8	14.2	71.0	50	10	US-10-009-792A-5
C 9	14	70.0	19	1	PCT-US03-04088-258
C 10	14	70.0	21	1	PCT-US03-04088-593
C 11	14	70.0	25	12	US-60-427-836-401411
C 12	13.8	69.0	25	6	US-09-660-222-20311
C 13	13.8	69.0	25	9	US-10-355-577-283954
C 14	13.8	69.0	25	12	US-60-427-808-239182
C 15	13.8	69.0	25	12	US-60-427-808-294455
C 16	13.8	69.0	25	12	US-60-427-808-546726
C 17	13.8	69.0	25	12	US-60-427-836-424019
C 18	13.6	68.0	20	6	US-09-964-059B-139
C 19	13.6	68.0	25	9	US-10-355-577-850409
C 20	13.6	68.0	25	12	US-60-427-808-374528

21	13.6	68.0	25	12	US-60-427-808-823538	Sequence 823538,
22	13.6	68.0	25	12	US-60-427-808-823539	Sequence 823539,
23	13.6	68.0	45	12	US-60-288-292-37984	Sequence 37984, A
24	13.4	67.0	25	9	US-10-355-577-386767	Sequence 386767,
25	13.4	67.0	25	9	US-10-355-577-386768	Sequence 386768,
26	13.4	67.0	25	9	US-10-355-577-654361	Sequence 654361,
27	13.4	67.0	46	10	US-10-199-209A-5	Sequence 5, Appli
28	13.2	66.0	25	7	US-09-953-570-1381	Sequence 1381, Ap
29	13.2	66.0	25	9	US-10-355-577-225795	Sequence 225795,
30	13.2	66.0	25	9	US-10-355-577-270910	Sequence 270910,
31	13.2	66.0	25	9	US-10-355-577-599429	Sequence 599429,
32	13.2	66.0	25	9	US-10-355-577-600356	Sequence 600356,
33	13.2	66.0	25	9	US-10-355-577-806473	Sequence 806473,
34	13.2	66.0	25	12	US-60-427-808-12321	Sequence 12321, A
35	13.2	66.0	25	12	US-60-427-808-252863	Sequence 252863,
36	13.2	66.0	25	12	US-60-427-808-252864	Sequence 252864,
37	13.2	66.0	25	12	US-60-427-808-295640	Sequence 295640,
38	13.2	66.0	25	12	US-60-427-836-276560	Sequence 276560,
39	13.2	66.0	25	12	US-60-427-836-296253	Sequence 296253,
40	13.2	66.0	25	12	US-60-427-836-342508	Sequence 342508,
41	13.2	66.0	25	12	US-60-427-836-342509	Sequence 342509,
42	13.2	66.0	26	9	US-10-089-177-1492	Sequence 1492, Ap
43	13.2	66.0	50	9	US-10-325-899-7814	Sequence 7814, Ap
44	13	65.0	19	1	PCT-US03-04088-22	Sequence 22, Appl
45	13	65.0	19	1	PCT-US03-04088-286	Sequence 286, Appl

ALIGNMENTS

RESULT 1
PCT-US03-04088-588/c
; Sequence 588, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 588
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-588

Query Match 80.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTGGCAG 20
 |||||
 Db 21 CTCTTCGCGGTGGCAG 6

RESULT 2

PCT-US03-04088-530/c
 ; Sequence 530, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 530
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-530

Query Match 80.0%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTGGCAG 20
 |||||
 Db 23 CTCTTCGCGGTGGCAG 8

RESULT 3

US-09-890-648-6
 ; Sequence 6, Application US/09890648
 ; GENERAL INFORMATION:
 ; APPLICANT: Bullerdiek, Jörn
 ; TITLE OF INVENTION: Preparation for The Prevention and/or Treatment
 ; TITLE OF INVENTION: of a Tissue Change of Mesenchymal Origin
 ; FILE REFERENCE: B3960PCT
 ; CURRENT APPLICATION NUMBER: US/09/890,648
 ; CURRENT FILING DATE: 2002-12-23
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: description of the artificial sequence: primer ADEIH13AS
 US-09-890-648-6

Query Match 74.0%; Score 14.8; DB 6; Length 31;
 Best Local Similarity 88.9%; Pred. No. 1.4e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGTGGCAG 20
 |||||
 Db 12 AACTCTTCGCGGTGGCAG 29

RESULT 4

US-10-299-054A-7701
 ; Sequence 7701, Application US/10299054A
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
 ; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/299,054A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 11910
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 7701
 ; LENGTH: 43
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis complete genome.
 ; FEATURE:
 ; LOCATION: (3056464)...(3056506)
 ; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 9331
 US-10-299-054A-7701

Query Match 74.0%; Score 14.8; DB 10; Length 43;
 Best Local Similarity 88.9%; Pred. No. 1.4e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGC 18
 |||||
 Db 24 CCAACTCTTCGCGGTAGC 41

RESULT 5

US-10-355-577-207601/c
 ; Sequence 207601, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 207601
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-355-577-207601

Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 2.8e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
 |||||
 Db 21 CCAACTCTTCAAGGGGGCA 3

RESULT 6

US-60-427-808-776553
 ; Sequence 776553, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20

```
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 776553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-776553

Query Match          71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTTCGCGGTGGCA 20
Db 6 CCAACTTCGCGGTGGCA 24

RESULT 7
US-09-462-405C-4
; Sequence 4, Application US/09462405C
; GENERAL INFORMATION:
; APPLICANT: Hillgenberg, Moritz
; APPLICANT: Loser, Peter
; APPLICANT: Schnieders, Frank
; APPLICANT: Sandig, Volker
; APPLICANT: Strauss, Michael
; TITLE OF INVENTION: Cloning Vectors for Producing Adenoviral Minimal Viruses
; FILE REFERENCE: 101195-13
; CURRENT APPLICATION NUMBER: US/09/462,405C
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: PCT/DE98/01940
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-462-405C-4

Query Match          71.0%; Score 14.2; DB 5; Length 34;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
Db 10 CCAACTCTACTCGTGGCA 28

RESULT 8
US-10-009-792A-5/c
; Sequence 5, Application US/10009792A
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JEONG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; FILE REFERENCE: HYLEP60.001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-009-792A-5
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Query Match          71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
Db 23 CCAGCTCTCTCGGGTGGCA 5

RESULT 9
PCT-US03-04088-258/c
; Sequence 258, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 258
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-258

Query Match          70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCGCGGTGGCAG 20
Db 19 CTTCGCGGTGGCAG 6

RESULT 10
PCT-US03-04088-593
; Sequence 593, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 593
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
PCT-US03-04088-593

Query Match          70.0%; Score 14; DB 1; Length 21;
Best Local Similarity 78.6%; Pred. No. 3.4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTTGCGGGTGGCAG 20
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Db 1 CUUCGGGUGGCGAG 14

RESULT 11
US-60-427-836-401411
; Sequence 401411, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 401411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-401411

Query Match          70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGGGGTGGCA 19
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Db 4 TCTTCGGGGTGGCA 17

RESULT 12
US-09-660-222-20311/c
; Sequence 20311, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 20311
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: TIGR HG2663-HT2759
US-09-660-222-20311

Query Match          69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGG 17
   |||||
Db 18 CCACCTCTTAGGGTGG 2

RESULT 13
US-10-355-577-283954
; Sequence 283954, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UL13
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 283954
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-283954

Query Match          69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGG 17
   |||||
Db 3 CCACCTCTTCGAGGAGG 19

RESULT 14
US-60-427-808-239182/c
; Sequence 239182, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 239182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-239182

Query Match          69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCAG 20
   |||||
Db 21 AGTCCTTCGGGTGGCAG 5

RESULT 15
US-60-427-808-294455/c
; Sequence 294455, Application US/60427808
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 294455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-294455

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Query Match      69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. NO. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      3 AACTCTTCGGGTGCA 19
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Db      21 AACTCTTCGAGGTAGCA 5

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Search completed: June 26, 2003, 04:15:16
Job time : 479.077 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
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37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR063830 Sequence
2	20	100.0	30	6	AR063829 Sequence
3	12	60.0	20	12	AB069038 Synthetic
4	12	60.0	28	9	S72525 TCR V gamma
5	12	60.0	30	9	HSTCRGV33
6	12	60.0	43	6	AX158160 Sequence
7	12	60.0	46	6	AX158162 Sequence
8	12	60.0	50	6	AX024597 Sequence
9	11	55.0	12	6	A14857 Nucleotide
10	11	55.0	15	6	AR056247 Sequence
11	11	55.0	15	6	AR114005 Sequence
12	11	55.0	18	6	A32455 Synthetic p
13	11	55.0	18	6	A32726 Synthetic d
14	11	55.0	18	6	I19611 Sequence 12
15	11	55.0	18	6	I84271 Sequence 42
16	11	55.0	20	6	A09892 Oligonucleo
17	11	55.0	20	6	A09923 Probe. 1/19
18	11	55.0	20	6	A14859 Nucleotide
19	11	55.0	20	6	AR002212 Sequence
20	11	55.0	20	6	E05218 Probe for g
21	11	55.0	20	6	E16501 PCR primer
22	11	55.0	21	6	AR129457 Sequence
23	11	55.0	21	6	AX110621 Sequence
24	11	55.0	22	6	AX110619 Sequence
25	11	55.0	24	6	A09925 Probe. 1/19
26	11	55.0	24	6	AR171201 Sequence
27	11	55.0	24	6	AX068559 Sequence
28	11	55.0	24	6	AX445836 Sequence
29	11	55.0	25	9	HS270340 Homo sapi
30	11	55.0	27	9	HSTCRGV24
31	11	55.0	30	9	HSTCRGV22
32	11	55.0	30	9	S72587 TCR gamma =
33	11	55.0	30	9	S72591 TCR gamma =
34	11	55.0	36	6	AR148975 Sequence
35	11	55.0	36	6	AR196827 Sequence
36	11	55.0	36	6	AX016752 Sequence
37	11	55.0	36	6	AX016769 Sequence
38	11	55.0	38	6	AR148976 Sequence
39	11	55.0	38	6	AR196828 Sequence
40	11	55.0	38	6	AX016753 Sequence
41	11	55.0	38	6	AX016770 Sequence
42	11	55.0	39	9	HSTCRGV35
43	11	55.0	42	6	AR163562 Sequence
44	11	55.0	49	6	E08684 Oligonucleo
45	11	55.0	49	6	E08686 Oligonucleo

ALIGNMENTS

RESULT 1	AR063830	Sequence 6 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063830	Sequence 6 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR063830	Sequence 6 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR063830	Sequence 6 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR063830.1	GI:59931138	20 bp	DNA	linear	PAT 29-SEP-1999
KEYWORDS	AR063830.1	GI:59931138	20 bp	DNA	linear	PAT 29-SEP-1999
SOURCE	Unknown.	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
ORGANISM	Unknown.	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
REFERENCE	1 (bases 1 to 20)	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
AUTHORS	Kim, N. Woo., Wu, P., Kealey, J. T., Pruzan, R. and Weinrich, S. L.	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
TITLE	Methods for detecting the RNA component of telomerase	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
JOURNAL	Patent: US 5846723-A 6 08-DEC-1998;	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999
FEATURES	Location/Qualifiers	Unknown.	20 bp	DNA	linear	PAT 29-SEP-1999

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/organism="unknown"
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Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCTTC 20
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Db 1 CTGACAGAGCCCAACTCTTC 20
    |||||

RESULT 2
AR063829
LOCUS      AR063829
DEFINITION Sequence 5 from patent US 5846723.
ACCESSION  AR063829
VERSION     AR063829.1 GI:5993137
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 5 08-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1. .30
            /organism="unknown"
BASE COUNT      6 a      10 c      9 g      5 t
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Query Match      100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCTTC 20
    |||||
Db 1 CTGACAGAGCCCAACTCTTC 20
    |||||

RESULT 3
AB069038
LOCUS      AB069038
DEFINITION Synthetic construct DNA, forward primer for human STS sts-A008J44
            at lp36.
ACCESSION  AB069038
VERSION     AB069038.1 GI:15129842
KEYWORDS   synthetic construct DNA.
SOURCE     artificial sequences.
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
TITLE      A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome lp35-p36
JOURNAL    Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
REFERENCE  2 (bases 1 to 20)
AUTHORS    Horii,A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="synthetic construct"

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1. .20
/db xref="taxon:32630"
/note="forward primer for human STS sts-A008J44 at lp36
sts-A008J44 obtained from clones B316C6, B132G19, B375M9,
Human BAC library RPCI-11"
BASE COUNT      4 a      8 c      1 g      7 t
ORIGIN
Query Match      60.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCCCAACTCTTC 20
    |||||
Db 2 GCCCAACTCTTC 13
    |||||

RESULT 4
S72525
LOCUS      S72525/c
DEFINITION TCR V gamma 9-T cell receptor gamma chain (V-J junction) [human,
            mRNA Partial Mutant, 28 nt].
ACCESSION  S72525
VERSION     S72525.1 GI:240432
KEYWORDS   Homo sapiens.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Holroyd,K.J., Tamura,N., Banks,T., Kirby,M., Okayama,H. and
            Crystal,R.G.
TITLE      Limited diversity of gamma delta T-cell antigen receptor junctional
            region sequences in individuals with sarcoidosis compared to broad
            diversity in normal subjects
JOURNAL    Trans. Assoc. Am. Physicians 103, 102-111 (1990)
MEDLINE    92087348
PUBMED     2151899
REMARK     GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbaq 72525] from the original journal article.
            This sequence comes from Figure 4.
FEATURES   Location/Qualifiers
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            1. .28
            /organism="Homo sapiens"
            /db xref="taxon:9606"
            <1. .>28
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            /note="T cell receptor gamma chain"
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            /note="This sequence comes from Figure 4; conceptual
            translation differs from the translation presented in the
            manuscript"
            /codon_start=2
            /product="T cell receptor gamma chain"
            /protein_id="AAB20598.2"
            /db_xref="GI:7717239"
            /translation="PLWEREELG"
BASE COUNT      5 a      4 c      13 g      6 t
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Query Match      60.0%; Score 12; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCCCAACTCTTC 20
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Db 28 GCCCAACTCTTC 17
    |||||

RESULT 5
HSTCRGV33/c
LOCUS      HSTCRGV33

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DEFINITION H.sapiens mRNA for rearranged TCR-gamma chain V region (VJ).
ACCESSION X69253
VERSION G69253.1 GI:510639
KEYWORDS J-region; N-region; T-cell receptor; T-cell receptor gamma chain;
V-region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hvas, J.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1992) J. Hvas, La Trobe University,
Neuroimmunology Lab., Dept. of Psych., La Trobe University,
Bundoora, Victoria 3083, AUSTRALIA
REFERENCE 2 (bases 1 to 30)
AUTHORS Hvas, J., Oksenberg, J.R., Fernando, R., Steinman, L. and Bernard, C.C.
TITLE Gamma delta T cell receptor repertoire in brain lesions of patients
with multiple sclerosis
JOURNAL J. Neuroimmunol. 46 (1-2), 225-234 (1993)
MEDLINE 93367035
PUBMED 8395544
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/isolate="MS patient SEL"
/db_xref="taxon:9606"
/clone="MSSSELBRA5G"
/tissue_type="brain"
misc_feature 1..11
/note="V-gamma-2 segment"
misc_feature 12..16
/note="N region"
misc_feature 17..30
/note="J-gamma-1.2 segment"
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Query Match 60.0%; Score 12; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCCCAACTCTTC 20
Db 27 GCCCAACTCTTC 16
RESULT 6
AX158160/c
LOCUS AX158160 43 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1488 from Patent WO0140521.
ACCESSION AX158160
VERSION AX158160.1 GI:14539491
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 1488 07-JUN-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="Nucleotide deleted between bases 18 and 19"
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/note="2 of 2 allelic variants (1487 is other entry)"

BASE COUNT 10 a 14 c 6 g 13 t
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Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACGAGCCCAA 14
Db 28 GACGAGCCCAA 17
RESULT 7
AX158162/c
LOCUS AX158162 46 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1490 from Patent WO0140521.
ACCESSION AX158162
VERSION AX158162.1 GI:14539493
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 1490 07-JUN-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACGAGCCCAA 14
Db 28 GACGAGCCCAA 17
RESULT 8
AX024597
LOCUS AX024597 50 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 13 from Patent WO0028021.
ACCESSION AX024597
VERSION AX024597.1 GI:10184737
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 50)
AUTHORS Turecek, P., Pannekoek, H., and Mertens, K.
TITLE A factor viii-polypeptide with factor viii:c-activity
JOURNAL Patent: WO 0028021-A 13 18-MAY-2000;
BAXTER AKTIENGESSELLSCHAFT (AT); TURECEK PETER (AT); SCHEIFLINGER
FRIEDRICH (AT); SCHWARZ HANS PETER (AT); LENTING PETRUS JOHANNES
(NL); MOURIK JAN AART VAN (NL); PANNEKOEK HANS (NL); MERTENS
KOENRAAD (NL)
FEATURES
Location/Qualifiers
1..50
/organism="synthetic construct"
/db_xref="taxon:32630"

SOURCE synthetic construct.
ORGANISM synthetic construct
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FEATURES
source
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCCA 13
|||||
Db 4 GACAGAGCCCCA 14

RESULT 14
I19611
LOCUS 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 12 from patent US 5510084.
ACCESSION I19611
VERSION I19611.1 GI:1599966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Cross, P., Allibert, P.A., Mandrand, B.P. and Dalbon, P.T.
TITLE Process for immobilizing a nucleic acid fragment by passive attachment to a solid substrate, the solid substrate thus obtained, and its use
JOURNAL Patent: US 5510084-A 12 23-APR-1996;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCCA 13
|||||
Db 4 GACAGAGCCCCA 14

RESULT 15
I84271
LOCUS 18 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 42 from patent US 5695926.
ACCESSION I84271
VERSION I84271.1 GI:3021791
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Cross, P., Allibert, P., Mallet, F., Mabilat, C. and Mandrand, B.
TITLE Sandwich hybridization assays using very short capture probes noncovalently bound to a hydrophobic support
JOURNAL Patent: US 5695926-A 42 09-DEC-1997;
FEATURES
source
1. .18
Location/Qualifiers
/organism="unknown" 2 t
BASE COUNT 5 a 7 c 4 g 2 t
ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCCA 13
|||||
Db 4 GACAGAGCCCCA 14

Search completed: June 23, 2003, 06:34:16
Job time : 234.051 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 977.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCACTTTC 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents NA, New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	23	1	PCT-US03-04088-522
C 2	19	95.0	21	1	PCT-US03-04088-540
C 3	19	95.0	21	1	PCT-US03-04088-544
C 4	19	95.0	21	1	PCT-US03-04088-548
C 5	19	95.0	21	1	PCT-US03-04088-552
C 6	19	95.0	21	1	PCT-US03-04088-556
C 7	19	95.0	21	1	PCT-US03-04088-560
C 8	18	90.0	19	1	PCT-US03-04088-23
C 9	18	90.0	19	1	PCT-US03-04088-287
C 10	14	70.0	25	12	US-60-427-808-47221
C 11	14	70.0	25	12	US-60-427-808-699316
C 12	14	70.0	25	12	US-60-427-808-529892
C 13	13	65.0	20	1	PCT-US02-21361-189
C 14	13	65.0	20	9	US-10-188-186-189
C 15	13	65.0	20	9	US-10-160-619-306
C 16	13	65.0	20	9	US-10-160-619-315
C 17	13	65.0	25	6	US-09-660-222-66821
C 18	13	65.0	25	6	US-09-660-222-66822
C 19	13	65.0	25	6	US-09-660-222-66827
C 20	13	65.0	25	6	US-09-660-222-66828

C 21	13	65.0	25	6	US-09-660-222-66829	Sequence 66829, A
C 22	13	65.0	25	9	US-10-355-577-281714	Sequence 281714, A
C 23	13	65.0	25	9	US-10-355-577-534052	Sequence 534052, A
C 24	13	65.0	25	12	US-60-427-808-2606	Sequence 2606, Ap
C 25	13	65.0	25	12	US-60-427-808-435724	Sequence 435724, A
C 26	13	65.0	25	12	US-60-427-808-467623	Sequence 467623, A
C 27	13	65.0	25	12	US-60-427-808-503841	Sequence 503841, A
C 28	13	65.0	25	12	US-60-427-836-9568	Sequence 9568, Ap
C 29	13	65.0	25	12	US-60-427-836-95550	Sequence 95550, A
C 30	13	65.0	25	12	US-60-427-836-198381	Sequence 198381, A
C 31	13	65.0	25	12	US-60-427-836-331174	Sequence 331174, A
C 32	12	60.0	24	9	US-10-293-338-4756	Sequence 4756, Ap
C 33	12	60.0	25	6	US-09-660-222-209	Sequence 209, App
C 34	12	60.0	25	6	US-09-660-222-27816	Sequence 27816, A
C 35	12	60.0	25	6	US-09-660-222-27829	Sequence 27829, A
C 36	12	60.0	25	6	US-09-660-222-28011	Sequence 28011, A
C 37	12	60.0	25	6	US-09-660-222-28022	Sequence 28022, A
C 38	12	60.0	25	7	US-09-953-570-9476	Sequence 9476, Ap
C 39	12	60.0	25	7	US-09-953-570-9478	Sequence 9478, Ap
C 40	12	60.0	25	7	US-09-954-445A-21329	Sequence 21329, A
C 41	12	60.0	25	9	US-10-355-577-72838	Sequence 72838, A
C 42	12	60.0	25	9	US-10-355-577-282353	Sequence 282353, A
C 43	12	60.0	25	9	US-10-355-577-515821	Sequence 515821, A
C 44	12	60.0	25	9	US-10-355-577-558628	Sequence 558628, A
C 45	12	60.0	25	12	US-60-427-808-48673	Sequence 48673, A

ALIGNMENTS

RESULT 1
PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 100.0%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
PCT-US03-04088-540/c
Sequence 540, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 540
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
NAME/KEY: misc feature
LOCATION: (20)-(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-544

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
PCT-US03-04088-548/c
Sequence 548, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc feature
LOCATION: (1)-(1)

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
PCT-US03-04088-540/c
Sequence 540, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 540
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc feature
LOCATION: (20)-(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-540

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 3
PCT-US03-04088-544
Sequence 544, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124

```
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  TGACAGAGCCCAACTCTTC 20
    |||||
Db   19 TGACAGAGCCCAACTCTTC 1
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```
RESULT 5
PCT-US03-04088-552
; Sequence 552. Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 552
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; FEATURE:
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
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```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  2  TGACAGAGCCCAACTCTTC 20
    |||||
Db   1  UGACAGAGCCCAACUCUC 19
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RESULT 6
PCT-US03-04088-556/c
; Sequence 556. Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 556
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 2'-deoxy
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NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-556

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 7
PCT-US03-04088-560
Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 8
PCT-US03-04088-23/c
Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 23
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-23

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGACAGAGCCCAACTCT 18
 Db 18 CTGACAGAGCCCAACTCT 1

RESULT 9
 PCT-US03-04088-287
 ; Sequence 287, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 287
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
 ; OTHER INFORMATION: region
 PCT-US03-04088-287

Query Match 90.0%; Score 18; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.1;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGACAGAGCCCAACTCT 18
 Db 2 CUGACAGAGCCCAACUCU 19

RESULT 10
 US-60-427-808-47221
 ; Sequence 47221, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 47221
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-47221

Query Match 70.0%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 AGAGCCCAACTCTT 19
 Db 2 AGAGCCCAACTCTT 15

RESULT 11
 US-60-427-808-699316
 ; Sequence 699316, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 699316
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-699316

Query Match 70.0%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GAGCCCAACTCTTC 20
 Db 3 GAGCCCAACTCTTC 16

RESULT 12
 US-60-427-836-529892/c
 ; Sequence 529892, Application US/60427836
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527
 ; CURRENT APPLICATION NUMBER: US/60/427,836
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 529892
 ; LENGTH: 25
 ; TYPE: DNA

; ORGANISM: Rattus norvegicus
US-60-427-836-52992

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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TCACAGAGCCCAAC 15
DB 14 TCACAGAGCCCAAC 1

RESULT 13

PCT-US02-21361-189
Sequence 189, Application PC/TUS0221361
GENERAL INFORMATION:
APPLICANT: Curagen Corporation, et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: PCT/US02/21361
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/304502
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 368
SOFTWARE: Custom
SEQ ID NO 189
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer

Query Match 65.0%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AGAGCCCAACTCT 18
DB 6 AGAGCCCAACTCT 18

RESULT 14

US-10-188-186-189
Sequence 189, Application US/10188186
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814

OY 6 AGAGCCCAACTCT 18
DB 6 AGAGCCCAACTCT 18

RESULT 15

US-10-160-619-306
Sequence 306, Application US/10160619
GENERAL INFORMATION:
APPLICANT: Agee, Michele
APPLICANT: Alsobrook, John
APPLICANT: Anderson, David
APPLICANT: Berghs, Constance
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Catterton, Elina
APPLICANT: DiPippo, Vincent
APPLICANT: Edinger, Shlomit
APPLICANT: Eisen, Andrew
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia
APPLICANT: Herrmann, John
APPLICANT: Hjalt, Tord
APPLICANT: Ji, Weizhen
APPLICANT: Kekuda, Ramesh
APPLICANT: Khrantsov, Nikolai
APPLICANT: Lepley, Denise
APPLICANT: Li, Li
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel
APPLICANT: Miller, Charles
APPLICANT: Millet, Isabelle
APPLICANT: Ort, Tatiana
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel

PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/304502
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 368
SOFTWARE: Custom
SEQ ID NO 189
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer

US-10-188-186-189
Query Match 65.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AGAGCCCAACTCT 18
DB 6 AGAGCCCAACTCT 18

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; APPLICANT: Rothenberg, Mark
; APPLICANT: Shency, Suresh
; APPLICANT: Shimkets, Richard
; APPLICANT: Smithson, Glennnda
; APPLICANT: Spaderna, Steven
; APPLICANT: Spytek, Kimberly
; APPLICANT: Stone, David
; APPLICANT: Vernet, Corine
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-377C
; CURRENT APPLICATION NUMBER: US/10/160,619
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,528
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 539
; SEQ ID NO 306
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer
US-10-160-619-306

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Query Match      65.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      6 AGAGCCCAACTCT 18

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Job time : 877.928 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCAACTTTC 20

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Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues.

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	30	1	PCT-US97-23619-5
4	20	100.0	30	11	US-08-770-564A-5
5	18	90.0	24	9	US-08-521-634-15
6	13	65.0	25	17	US-09-396-1965-124326
7	13	65.0	25	17	US-09-396-1965-124326
8	13	65.0	25	26	US-09-660-220-66821
9	13	65.0	25	26	US-09-660-220-66822
10	13	65.0	25	26	US-09-660-220-66827
11	13	65.0	25	26	US-09-660-220-66828
12	13	65.0	25	26	US-09-660-220-66829
13	13	65.0	25	36	US-09-956-584-314490
14	13	65.0	25	36	US-09-956-584-314500
15	13	65.0	25	67	US-60-234-017-309805
16	13	65.0	25	67	US-60-234-017-309812
17	13	65.0	25	79	US-60-353-987-281714
18	13	65.0	25	79	US-60-353-987-534052
19	13	65.0	42	29	US-09-724-750-18382
20	13	65.0	42	61	US-60-171-431-18382
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					Sequence 124326, A
					Sequence 66821, A
					Sequence 66822, A
					Sequence 66827, A
					Sequence 66828, A
					Sequence 66829, A
					Sequence 314490,
					Sequence 314500,
					Sequence 309805,
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					Sequence 18382, A
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					Sequence 38, Appli

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; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 16ab"
PCT-US97-23619-6

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
PCT-US97-23619-5

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Sequence 5, Application PC/TUS9723619
GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619

FILING DATE: Not yet assigned

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,564

FILING DATE: 20-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,565

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 15389-27PC

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY:

LOCATION: 1..30

OTHER INFORMATION: /note= "oligo 16"

PCT-US97-23619-5

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 4

US-08-770-564A-5

Sequence 5, Application US/08770564A

GENERAL INFORMATION:

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ron

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Inhibitory Polynucleotides Directed

TITLE OF INVENTION: Against the RNA Component of Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,564A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002200US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-564A-5

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 5

US-08-521-634-15/c

Sequence 15, Application US/08521634

GENERAL INFORMATION:

APPLICANT: Villegonteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/521,634

FILING DATE: 31-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,115

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match          90.0%; Score 18; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
DB 24 GACAGAGCCCAACTCTTC 7

RESULT 6
US-09-396-196F-124326
; Sequence 124326, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-124326

Query Match          65.0%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCA 14
DB 2 TGACAGAGCCCA 14

RESULT 7
US-09-396-196G-124326
; Sequence 124326, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124326

Query Match          65.0%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCA 14
DB 2 TGACAGAGCCCA 14

RESULT 8
US-09-660-220-66821/c
; Sequence 66821, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66821
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66821

Query Match          65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTC 17
DB 16 CAGAGCCCACTC 4

RESULT 9
US-09-660-220-66822/c
; Sequence 66822, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66822

Query Match          65.0%; Score 13; DB 26; Length 25;
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Best Local Similarity 100.0%; Pred. No. 3.7e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 5 CAGAGCCCAACTC 17
DB 13 CAGAGCCCAACTC 1

RESULT 10
US-09-660-220-66827/c
; Sequence 66827, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66827
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66827

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 19 CAGAGCCCAACTC 7

RESULT 11
US-09-660-220-66828/c
; Sequence 66828, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66828

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 25 CAGAGCCCAACTC 13

RESULT 12
US-09-660-220-66829/c
; Sequence 66829, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66829

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 25 CAGAGCCCAACTC 13

RESULT 13
US-09-956-584-314490
; Sequence 314490, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 314490
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-314490

Query Match 65.0%; Score 13; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
DB 1 CTGACAGAGCCCA 13

RESULT 14
US-09-956-584-314500
; Sequence 314500, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 314500
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-314500
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US-09-956-584-314500

Query Match 65.0%; Score 13; DB 36; Length 25;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
|||||
Db 6 CTGACAGAGCCCA 18

RESULT 15

US-60-234-017-309805

; Sequence 309805, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; TITLE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 309805

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AW049747

US-60-234-017-309805

Query Match 65.0%; Score 13; DB 67; Length 25;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
|||||
Db 1 CTGACAGAGCCCA 13

Search completed: June 23, 2003, 16:08:19
Job time : 1678.53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCAACTTTC 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12	60.0	31	9	US-09-288-971-6
2	12	60.0	31	9	US-09-288-971-10
3	11	55.0	18	10	US-09-969-373-3187
c 4	11	55.0	21	9	US-10-222-334-65
5	11	55.0	24	9	US-09-940-185-2291
c 6	11	55.0	24	10	US-09-898-779-110
7	11	55.0	25	9	US-09-992-665-205
8	11	55.0	25	9	US-10-098-263B-110352
9	11	55.0	26	10	US-09-118-276-16
c 10	11	55.0	36	9	US-09-986-118A-24
c 11	11	55.0	36	9	US-09-824-017-25
c 12	11	55.0	38	9	US-09-986-118A-25
c 13	11	55.0	38	9	US-09-818-875-1383
14	10	50.0	17	9	US-09-818-875-1384
c 15	10	50.0	17	9	US-09-818-875-1387
c 16	10	50.0	17	9	US-09-818-875-1388
c 17	10	50.0	17	9	US-09-818-875-1388
c 18	10	50.0	19	9	US-10-093-958-22
c 19	10	50.0	19	9	US-10-291-022-2

c 20	10	50.0	20	9	US-10-090-011-45
21	10	50.0	20	9	US-09-915-814-161
22	10	50.0	20	10	US-09-263-959-1126
23	10	50.0	21	9	US-09-853-526-420
24	10	50.0	21	9	US-10-082-804-3
25	10	50.0	21	9	US-09-909-567B-23
26	10	50.0	21	9	US-10-085-906-387
27	10	50.0	21	10	US-09-901-484A-420
c 28	10	50.0	23	9	US-10-090-887-8
c 29	10	50.0	23	10	US-09-808-382-4
30	10	50.0	24	9	US-09-940-185-2918
31	10	50.0	25	8	US-08-647-444-5
c 32	10	50.0	25	9	US-10-098-263B-5700
33	10	50.0	25	9	US-10-098-263B-12238
34	10	50.0	25	9	US-10-098-263B-34264
c 35	10	50.0	25	9	US-10-098-263B-42033
c 36	10	50.0	25	9	US-10-098-263B-42034
c 37	10	50.0	25	9	US-10-098-263B-44063
c 38	10	50.0	25	9	US-10-098-263B-49892
39	10	50.0	25	9	US-10-098-263B-56499
40	10	50.0	25	9	US-10-098-263B-56500
41	10	50.0	25	9	US-10-098-263B-72819
42	10	50.0	25	9	US-10-098-263B-78124
c 43	10	50.0	25	9	US-10-098-263B-79153
c 44	10	50.0	25	9	US-10-098-263B-79154
45	10	50.0	25	9	US-10-098-263B-83271

ALIGNMENTS

RESULT 1

US-09-288-971-6/c
; Sequence 6, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorce, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-6

Query Match 60.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
DB 28 CTGACAGAGCCC 17

RESULT 2

US-09-288-971-10
; Sequence 10, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorce, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10

Query Match

Best Local Similarity 60.0%; Score 12; DB 9; Length 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-288-971-10
QY 1 CTGACAGAGCC 12
DB 4 CTGACAGAGCC 15

RESULT 3

US-09-969-373-3187
; Sequence 3187, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eifert, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US/09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US/09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3187
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3187

Query Match

Best Local Similarity 55.0%; Score 11; DB 10; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-969-373-3187
QY 9 GCCCACTCTT 19
DB 7 GCCCACTCTT 17

RESULT 4

US-10-222-334-65/c
; Sequence 65, Application US/10222334
; Publication No. US20030073116A1
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Gallia
; APPLICANT: Tsai, Han-Mou
; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
; FILE REFERENCE: UM-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/312,834
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-222-334-65

Query Match

Best Local Similarity 55.0%; Score 11; DB 9; Length 21;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-940-185-2291

US-09-940-185-2291
; Sequence 2291, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2291
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2291

Query Match

Best Local Similarity 55.0%; Score 11; DB 9; Length 24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-940-185-2291
QY 2 TGACAGAGCC 12
DB 7 TGACAGAGCC 17

RESULT 6

US-09-898-779-110/c
; Sequence 110, Application US/09898779
; Patent No. US20020106657A1
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE REFERENCE: 18810-82302
; CURRENT APPLICATION NUMBER: US/09/898,779
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/347,114
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-779-110

Query Match

Best Local Similarity 55.0%; Score 11; DB 10; Length 24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-898-779-110
QY 1 CTGACAGAGCC 11
DB 19 CTGACAGAGCC 9

RESULT 7

US-09-992-665-205
 ; Sequence 205, Application US/09992665
 ; Publication No. US20030092009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaia Palm
 ; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: CEMINES.002A
 ; CURRENT APPLICATION NUMBER: US/09/992,665
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: 60/249,508
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 205
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-09-992-665-205

Query Match 55.0%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13

DB 3 GACAGAGCCCA 13

RESULT 8

US-10-098-263B-110352
 ; Sequence 110352, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 110352
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-110352

Query Match 55.0%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20

DB 3 CCCAACTCTTC 13

RESULT 9

US-09-118-276-16
 ; Sequence 16, Application US/09118276
 ; Patent No. US20010011381A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BABYCHUK, ELENA;
 ; APPLICANT: KUSHNIR, SERGEI;
 ; APPLICANT: DE BLOCK, MARC;
 ; APPLICANT: INZE, DIRK
 ; TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED
 ; TITLE OF INVENTION: CELL DEATH IN EUKARYOTIC CELLS

NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SIXBEY, FRIEDMAN, LEEDOM, & FERGUSON
 STREET: 8180 GREENSBORO DRIVE, SUITE 800
 CITY: MCLEAN,
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3-1/2" DISKETTE
 COMPUTER: IBM-COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/118,276
 FILING DATE: 17-JUL-1998
 PRIOR APPLICATION DATA: NONE
 ATTORNEY/AGENT INFORMATION:
 NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH H.
 REGISTRATION NUMBER: 31,196; 43,077
 REFERENCE/DOCKET NUMBER: 6201-0003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 790-9110
 TELEFAX: (703) 883-0370
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 BASES
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 US-09-118-276-16

Query Match 55.0%; Score 11; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20

DB 11 CCCAACTCTTC 21

RESULT 10

US-09-824-017-24/c
 ; Sequence 24, Application US/09824017
 ; Publication No. US20020197668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BURGER, Alexander
 ; HALLER, Michael
 ; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 ; FORMULATIONS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/824,017
 FILING DATE: 03-Apr-2001
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,896
 FILING DATE: 1998-02-20
 ATTORNEY/AGENT INFORMATION:
 NAME: Sandercock, Colin G.
 REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-824-017-24

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
DB 28 GACAGAGCCCA 18

RESULT 11

US-09-986-118A-24/c
Sequence 24, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-No. US20030021806A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-986-118A-24

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACAGAGCCCA 13
DB 28 GACAGAGCCCA 18

RESULT 12

US-09-824-017-25/c
Sequence 25, Application US/09824017
Publication No. US20020197668A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-824-017-25

Query Match 55.0%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
DB 36 GACAGAGCCCA 26

RESULT 13

US-09-986-118A-25/c
Sequence 25, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY & LARDNER
;; STREET: 3000 K Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20007-5109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/986,118A
;; FILING DATE: 07-NO. US20030021806A1-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/026,896
;; FILING DATE: <Unknown>
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sandercock, Colin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37067/102
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;;
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Primer"
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-986-118A-25

Query Match 55.0%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
Db 36 GACAGAGCCCA 26

RESULT 14

US-09-818-875-1383
; Sequence 1383, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1383
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-818-875-1383

Query Match 50.0%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCCCAACT 16
Db 1 GAGCCCAACT 10

RESULT 15

US-09-818-875-1384/c
; Sequence 1384, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1384

Query Match 50.0%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCCCAACT 16
Db 17 GAGCCCAACT 8

Search completed: June 23, 2003, 20:01:30
Job time : 160.717 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTTTC 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B-COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A-COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-08-770-565-6	Sequence 6, Appli
2	20	100.0	30	US-08-770-565-5	Sequence 5, Appli
3	14	70.0	26	US-08-974-180-33	Sequence 33, Appli
4	11	55.0	15	US-08-292-620A-451	Sequence 451, App
5	11	55.0	15	US-09-071-845-451	Sequence 451, App
6	11	55.0	18	US-08-273-776-12	Sequence 12, Appl
7	11	55.0	18	US-08-255-892-42	Sequence 42, Appl
8	11	55.0	20	US-08-358-993-2	Sequence 2, Appli
9	11	55.0	20	US-08-913-547-3	Sequence 3, Appli
10	11	55.0	21	US-08-927-219-29	Sequence 29, Appl
11	11	55.0	24	US-09-347-114A-110	Sequence 110, App
12	11	55.0	36	US-08-944-368A-24	Sequence 24, Appl
13	11	55.0	36	US-09-820-764-24	Sequence 24, Appl
14	11	55.0	38	US-08-944-368A-25	Sequence 25, Appl
15	11	55.0	38	US-09-820-764-25	Sequence 25, Appl
16	11	55.0	42	US-09-051-363-23	Sequence 23, Appl
17	10	50.0	17	US-08-292-620A-1733	Sequence 1733, Ap
18	10	50.0	17	US-08-071-845-1733	Sequence 1733, Ap
19	10	50.0	17	US-08-584-040-5345	Sequence 5345, Ap
20	10	50.0	18	US-08-599-252-1	Sequence 1, Appli
21	10	50.0	18	US-08-436-074-1	Sequence 1, Appli
22	10	50.0	18	US-09-050-159-5	Sequence 5, Appli
23	10	50.0	18	PCT-US96-06352-1	Sequence 1, Appli
24	10	50.0	18	PCT-US96-06583-1	Sequence 1, Appli
25	10	50.0	20	US-08-770-565-7	Sequence 7, Appli
26	10	50.0	20	US-08-911-894-75	Sequence 75, Appl
27	10	50.0	20	US-08-338-579A-49	Sequence 49, Appl

28	10	50.0	20	4	US-09-545-686-26	Sequence 26, Appli
29	10	50.0	20	5	PCT-US94-09851-49	Sequence 49, Appli
30	10	50.0	21	3	US-09-009-913-250	Sequence 250, App
31	10	50.0	21	4	US-09-338-907-420	Sequence 420, App
32	10	50.0	21	4	US-09-218-207-420	Sequence 420, App
33	10	50.0	21	4	US-08-669-656A-24	Sequence 24, Appli
34	10	50.0	24	1	US-07-965-274-2	Sequence 2, Appli
35	10	50.0	24	1	US-08-203-905B-25	Sequence 25, Appli
36	10	50.0	27	3	US-08-783-853A-67	Sequence 67, Appli
37	10	50.0	27	3	US-09-248-571-6	Sequence 6, Appli
38	10	50.0	27	4	US-09-344-050-67	Sequence 67, Appli
39	10	50.0	27	4	US-09-553-736-6	Sequence 6, Appli
40	10	50.0	28	4	US-09-150-622A-4	Sequence 4, Appli
41	10	50.0	30	3	US-08-577-121-47	Sequence 47, Appli
42	10	50.0	30	4	US-08-985-700-47	Sequence 47, Appli
43	10	50.0	30	5	PCT-US95-16916-47	Sequence 47, Appli
44	10	50.0	38	2	US-08-292-620A-2026	Sequence 2026, Ap
45	10	50.0	38	2	US-08-292-620A-2181	Sequence 2181, Ap

ALIGNMENTS

RESULT 1
US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2

US-08-770-565-5
 ; Sequence 5, Application US/08770565
 ; Patent No. 5846723
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Nam Woo
 ; APPLICANT: Wu, Fred
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ronald
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Methods for Detecting the RNA Component of
 ; TITLE OF INVENTION: Telomerase
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,565
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002300US
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-770-565-5

Query Match 100.0%; Score 20; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20
 Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3

US-08-974-180-33/c
 ; Sequence 33, Application US/08974180
 ; Patent No. 6025194
 ; GENERAL INFORMATION:
 ; APPLICANT: Funk, Walter
 ; TITLE OF INVENTION: Methods for Modulating and Identifying
 ; TITLE OF INVENTION: Cellular Senescence
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Geron Corporation
 ; STREET: 230 Constitution Drive
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,180
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaster, Kevin R.
 ; REGISTRATION NUMBER: 32,704
 ; REFERENCE/DOCKET NUMBER: 206
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 473-7779
 ; TELEFAX: (650) 473-8654
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..26
 ; OTHER INFORMATION: /note= "primer hTR S328"
 ; US-08-974-180-33

Query Match 70.0%; Score 14; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAA 14
 Db 14 CTGACAGAGCCCAA 1

RESULT 4

US-08-292-620A-451
 ; Sequence 451, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Sean Sullivan
 ; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: INTRACELLULAR ADHESION
 ; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
 ; NUMBER OF SEQUENCES: 2390
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/292,620A
 ; FILING DATE: August 17, 1994
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-451

Query Match 55.0%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 10 CCCAACTCTTC 20
Db 1 CCCAACUCUC 11

RESULT 5
US-09-071-845-451
Sequence 451, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwigen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-451
Query Match 55.0%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 10 CCCAACTCTTC 20
Db 1 CCCAACUCUC 11
RESULT 6
US-08-273-776-12
Sequence 12, Application US/08273776
Patent No. 5510084
GENERAL INFORMATION:
APPLICANT: Cros, Phillippe
APPLICANT: Allibert, Patrice Andre
APPLICANT: Dalbon, Pascal Thierry
TITLE OF INVENTION: Process for Immobilizing a Nucleic Acid
TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff and Berridge
STREET: 700 S. Washington St.
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,776
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,953
FILING DATE: 17-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB28083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

two

US-08-273-776-12

Query Match 55.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 4 GACAGAGCCCA 14

RESULT 7

US-08-255-892-42
; Sequence 42, Application US/08255892
; Patent No. 5695926
; GENERAL INFORMATION:
; APPLICANT: CROS, PHILIPPE
; APPLICANT: ALLIBERT, PATRICE
; APPLICANT: MALLAT, FRANCOIS
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
; TITLE OF INVENTION: TECHNIQUE
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,892
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/834,543
; FILING DATE: 11-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.
; REGISTRATION NUMBER: 23,048
; REFERENCE/DOCKET NUMBER: 1032/94109
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-255-892-42

Query Match 55.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 4 GACAGAGCCCA 14

RESULT 8

US-08-358-995-2/c
; Sequence 2, Application US/08358995

; Patent No. 5741638
; GENERAL INFORMATION:
; APPLICANT: AKIO YAMANE
; TITLE OF INVENTION: Microtiter Well For Detecting
; TITLE OF INVENTION: Nucleic Acid
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,995
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,572
; FILING DATE: January 14, 1993
; APPLICATION NUMBER: 07/722,673
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "having biotin at
; OTHER INFORMATION: 5' end with a spacer"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:

```
;
;
; ISSUE:
; DATE:
; PAGES:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-358-995-2

Query Match          55.0%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
Db 18 GACAGAGCCCA 8

RESULT 9
US-08-913-547-3
; Sequence 3, Application US/08913547A
; Patent No. 6027891
; GENERAL INFORMATION:
; APPLICANT: VON KNEBEL-DOBRITZ, Magnus
; APPLICANT: WERNER, Stefano
; APPLICANT: EMERICH, Florian
; TITLE OF INVENTION: A METHOD OF EARLY DETECTION OF
; TITLE OF INVENTION: HPV-ASSOCIATED CARCINOMAS AND EXTREME DYSPLASIAS
; TITLE OF INVENTION: CAUSED BY HPV
; FILE REFERENCE: 035280028999
; CURRENT APPLICATION NUMBER: US/08/913,547A
; CURRENT FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-547-3

Query Match          55.0%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
Db 3 GACAGAGCCCA 13

RESULT 10
US-08-927-219-29
; Sequence 29, Application US/08927219
; Patent No. 6197533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisha
; APPLICANT: Katsaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
```

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;
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,219
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,679
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,056
; FILING DATE: 02-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,719
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-927-219-29

Query Match          55.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCC 12
Db 5 TGACAGAGCCC 15

RESULT 11
US-09-347-114A-110/c
; Sequence 110, Application US/09347114A
; Patent No. 6297014
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; TITLE OF INVENTION: No. 6297014-responsiveness to Statin Drug Treatment
; FILE REFERENCE: P07 41878
; CURRENT APPLICATION NUMBER: US/09/347,114A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-114A-110

Query Match          55.0%; Score 11; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCC 11
Db 19 CTGACAGAGCC 9

RESULT 12
```

US-08-944-368A-24/c
; Sequence 24, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-944-368A-24

Query Match 55.0%; Score 11; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
|||
Db 28 GACAGAGCCCA 18

RESULT 13
US-09-820-764-24/c
; Sequence 24, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-820-764-24

Query Match 55.0%; Score 11; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
|||
Db 28 GACAGAGCCCA 18

RESULT 14
US-08-944-368A-25/c
; Sequence 25, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-944-368A-25

Query Match 55.0%; Score 11; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 36 GACAGAGCCCA 26

RESULT 15

US-09-820-764-25/C
; Sequence 25, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO.: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-820-764-25

Query Match 55.0%; Score 11; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 36 GACAGAGCCCA 26

Search completed: June 23, 2003, 10:17:05
Job time : 31.3147 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N Geneseq_101002.*

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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- 16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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- 18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAV41173	RNA component of h
2	20	100.0	30	AAV41172	RNA component of h
C 3	14	70.0	26	AAV7131	PCR primer hTR S32
C 4	14	70.0	30	AAA61649	Mouse Elf-1 revers
5	12	60.0	20	ABL43397	Human chromosome 1
6	12	60.0	21	AZ233852	Rye microsatellit
7	12	60.0	21	AX36927	S. cereale microsa
8	12	60.0	24	AAV36173	PCR primer used to
C 9	12	60.0	43	AAI74547	Human silent SNP c

C 10	12	60.0	46	22	AAI74549	Human silent SNP c
C 11	12	60.0	50	21	AAV40237	Construct pc2-m9#5
C 12	11	55.0	13	23	ABF03254	Oligonucleotide SE
C 13	11	55.0	13	23	ABF03255	Oligonucleotide SE
C 14	11	55.0	13	23	ABH33140	Oligonucleotide SE
C 15	11	55.0	13	23	ABH33141	Oligonucleotide SE
C 16	11	55.0	15	16	AAV52289	Mouse ICAM hammerh
C 17	11	55.0	18	13	AAQ20414	Detection probe #2
C 18	11	55.0	18	14	AAQ36192	Detection probe fo
C 19	11	55.0	20	10	AAV97152	HPV-16 primer (694
C 20	11	55.0	20	10	AAV94234	Sequence of probe
C 21	11	55.0	20	17	AAV36613	s' primer for huma
C 22	11	55.0	20	22	AAV52648	Human diacylglycer
C 23	11	55.0	21	19	AAV52648	Hepatocyte nuclear
C 24	11	55.0	21	21	AAV77184	Human biallelic ma
C 25	11	55.0	21	22	AAH01363	aac(3')-IIB resist
C 26	11	55.0	21	22	AAV95841	Human gene single
C 27	11	55.0	21	24	ABA91189	Collectin PCR prim
C 28	11	55.0	22	22	AAH01361	aac(3')-IIB resist
C 29	11	55.0	23	21	AAV09876	Human papillomavir
C 30	11	55.0	24	10	AAV97159	Sequence of probe
C 31	11	55.0	24	10	AAV94236	Primer #106. Homo
C 32	11	55.0	24	22	AAV64166	Sequence of probe
C 33	11	55.0	24	24	ABQ02284	Oligonucleotide ad
C 34	11	55.0	24	24	ABQ08497	Oligonucleotide ad
C 35	11	55.0	24	24	ABQ08538	Oligonucleotide ad
C 36	11	55.0	25	16	AAQ87036	Oligonucleotide pr
C 37	11	55.0	25	24	ABT03684	Human NeuroDI gene
C 38	11	55.0	26	21	AAZ60622	PCR primer used to
C 39	11	55.0	30	16	AAQ91372	PCR primer for Al.
C 40	11	55.0	36	20	AAZ23409	HPV16L1E7 fusion p
C 41	11	55.0	36	20	AAZ23421	HPV16L1E7 fusion p
C 42	11	55.0	36	20	AAV37586	Human papilloma vi
C 43	11	55.0	36	21	AAZ48194	HPV 16 L1 expressi
C 44	11	55.0	38	20	AAZ23410	HPV16L1E7 fusion p
C 45	11	55.0	38	20	AAZ23422	HPV16L1E7 fusion p

ALIGNMENTS

RESULT 1	AAV41173	AAV41173 standard; DNA; 20 BP.
ID	AAV41173	standard; DNA; 20 BP.
XX	AAV41173;	
AC	AAV41173;	
XX	08-OCT-1998	(first entry)
DT	08-OCT-1998	(first entry)
XX	RNA component of human telomerase (hTR) antisense oligo 16ab.	
DE	RNA component; human telomerase; antisense oligonucleotide; infection;	
XX	neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;	
KW	contraception; sterlisation; immunosuppression; therapeutic; hTR;	
KW	immune system down-regulation; anti-inflammatory therapy; ss.	
XX	Synthetic.	
OS	Homo sapiens.	
XX	WO9828442-A1.	
XX	02-JUL-1998.	
PD	19-DEC-1997;	97WO-US23619.
XX	20-DEC-1996;	96US-0770565.
XX	20-DEC-1996;	96US-0770564.
PA	(GERO-) GERON CORP.	
XX	Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;	
XX	WPI; 1998-377670/32.	

XX New polynucleotide(s) antisense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
SQ Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
|||||
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
AAV41172
ID AAV41172 standard; DNA; 30 BP.
AC AAV41172;
XX
XX 08-OCT-1998 (first entry)
DT
DE RNA component of human telomerase (hTR) antisense oligo 16.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9828442-A1.
FN
XX 02-JUL-1998.
PD
XX 19-DEC-1997; 97WO-US23619.
PF
XX 20-DEC-1996; 96US-0770565.
PR
XX 20-DEC-1996; 96US-0770564.
PR
XX (GERO-) GERON CORP.
PA
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
PI WPI; 1998-377670/32.
XX
XX

PT New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ Query Match 100.0%; Score 20; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
|||||
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
AAV77131/c
ID AAX77131 standard; DNA; 26 BP.
XX
XX AAX77131;
XX
XX 03-AUG-1999 (first entry)
DT
XX
XX PCR primer hTR S328.
DE
XX Cellular senescence; modulator; GC6 gene; senescent gene expression;
KW pGC6; human; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO9925878-A2.
PN
XX 27-MAY-1999.
PD
XX 19-NOV-1998; 98WO-US24996.
PF
XX 19-NOV-1997; 97US-0974180.
PR
XX (GERO-) GERON CORP.
PA
XX Funk W;
PI WPI; 1999-347496/29.
DR
XX New human GC6 gene, useful for identifying agents for treating
PT diseases and/or conditions associated with cell senescence
XX
XX Example 5; Page 74; 79pp; English.
XX

CC The invention relates to methods for modulating and identifying cellular
 CC senescence. Recombinant expression vectors comprising a recombinant
 CC polynucleotide corresponding to a polynucleotide in a human GC6 gene, are
 CC useful for altering senescent gene expression. The vectors and host cells
 CC comprising the vectors are useful for identifying agents that prevent or
 CC modulate senescent gene expression. The polynucleotides are useful for
 CC producing the protein, pGC6 and nucleic acid derivatives. The proteins
 CC encoded are useful for raising antibodies specific for pGC6, which are
 CC useful for isolating pGC6, and for detecting cells comprising pGC6 in
 CC complex cell mixtures. The characterization of the polynucleotides enable
 CC the identification of therapeutic agents that identify and distinguish
 CC between young and senescent cells. This enables treatment of aging
 CC diseases induced or exacerbated by cellular senescence.

XX Sequence 26 BP; 1 A; 8 C; 9 G; 8 T; 0 other;

Query Match 70.0%; Score 14; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 69;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAA 14

DB 14 CTGACAGAGCCCAA 1

RESULT 4

AAA61649/c

ID AAA61649 standard; DNA; 30 BP.

XX

AC AAA61649;

XX

DT 23-OCT-2000 (first entry)

XX

DE Mouse Elf-1 reverse PCR primer.

XX

KW Elf-1; mouse; transcriptional regulatory factor; rat;

KW Polymorphic variant; immunological disease; allergic disease;

KW PCR primer; ss.

XX

OS Mus sp.

XX

PN JP2000135088-A.

XX

PD 16-MAY-2000.

XX

PF 30-OCT-1998; 98JP-0309595.

XX

PR 30-OCT-1998; 98JP-0309595.

XX

PA (ASAK) ASAHI BREWERIES LTD.

XX

DR WPI; 2000-425802/37.

XX

PT A transcription regulating factor Elf-1 cDNA and its polymorphism -

XX

PS Example 1; Page 4; 2ipp; Japanese.

XX

CC The invention relates to three polymorphic variants of a rat
 CC transcriptional regulatory factor Elf-1 (AA03190-803192) and nucleic
 CC acids encoding them (AAA61645-A61647). The invention also encompasses
 CC the use of Elf-1 for regulating the transcription of a gene in an
 CC expression vector. The cDNA encoding rat Elf-1 variant #1 (AAA61645)
 CC was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1
 CC cDNA, and the rat Elf-1 variant #2 and #3 cDNAs (AAA61646-A61647) were
 CC subsequently isolated. The Elf-1 cDNA and protein sequences are
 CC potentially useful for the prevention and treatment of immunological and
 CC allergic diseases mediated by Elf-1. Sequences AAA61648-A61649 represent
 CC mouse Elf-1 PCR primers used in an exemplification of the invention to
 CC isolate rat Elf-1 variant #1 cDNA.

XX Sequence 30 BP; 9 A; 4 C; 7 G; 10 T; 0 other;

Query Match

70.0%; Score 14; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 69;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTT 19

DB 19 AGAGCCCAACTCTT 6

RESULT 5

ABL43397

ID ABL43397 standard; DNA; 20 BP.

XX

AC ABL43397;

XX

DT 11-APR-2002 (first entry)

XX

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:441.

XX

KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
 genome; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN JP2001321190-A.

XX

PD 20-NOV-2001.

XX

PF 12-MAR-2001; 2001JP-0068285.

XX

PR 10-MAR-2000; 2000JP-0066716.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

PA (GENO-) GENOTEX YG.

XX

DR WPI; 2002-144136/19.

XX

PT Arraying genome clones -

XX

PS Claim 4; Page 13; 528pp; Japanese.

XX

CC The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the reactant;
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention.

XX Sequence 20 BP; 4 A; 8 C; 1 G; 7 T; 0 other;

Query Match 60.0%; Score 12; DB 24; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20

DB 2 GCCCAACTCTTC 13

```

RESULT 6
AAZ23852
ID AAZ23852 standard; DNA; 21 BP.
XX
XX
AC AAZ23852;
XX
DT 21-JAN-2000 (first entry)
XX
DE Rye microsatellite marker 13 PCR primer 2.
XX
XX Microsatellite marker; rye; hypervariable genomic region; Poaceae;
KW Triticeae; breeding program; DNA fingerprinting; variety; detection;
KW self pollination; cross pollination; cytoplasmic line; genetic mapping;
KW polymorphism; PCR primer; ss.
XX
XX Synthetic.
OS Secale cereale.
XX
XX DE19811506-A1.
XX
XX 21-OCT-1999.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX WPI; 1999-591715/51.
XX
XX New microsatellite markers for rye and closely related grasses, used
PT for genetic analysis and in breeding
XX
XX Claim 6; Page 27; 28pp; German.
XX
XX This invention describes novel microsatellite markers (MSM), based on
CC the hypervariable genomic regions of rye (Secale cereale) and of plants
CC from the tribes Triticeae and Poaceae. MSM, which are new genetic markers
CC for rye and closely related species, are used for genetic analysis and
CC in breeding programs. Typical applications are in DNA fingerprinting;
CC identification of varieties; detection of self and cross pollination;
CC characterization of cytoplasmic lines, and genetic mapping (of mono- or
CC poly-genic traits). MSM show a higher degree of polymorphism than known
CC markers (both within and between different rye varieties and lines); can
CC be detected by polymerase chain reaction, so that even very small
CC samples may be analyzed, and generate many alleles per marker locus.
CC AAZ23827-223886 represent the microsatellite marker PCR primers
CC described in the method of the invention.
XX
XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
SQ
Query Match 60.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 7
AAZ36927
ID AAZ36927 standard; DNA; 21 BP.
XX
XX
AC AAZ36927;
XX
DT 02-JUL-1999 (first entry)
XX
XX S. cereale microsatellite marker PCR primer 26.
XX
XX Microsatellite; marker; PCR primer; rye; plant; Triticeae; Poaceae;
KW sample sequence repeat; SSR; sequence tag site; STS; genetic analysis;
KW DNA fingerprinting; variety identification; self fertilization;

```

```

KW detection; cross fertilization; cytological line; gene mapping;
XX monogenic trait; polygenic trait; ss.
XX
XX Synthetic.
OS Secale cereale.
XX
XX DE19835109-A1.
XX
XX 15-APR-1999.
XX
XX 04-AUG-1998; 98DE-1035109.
XX
XX 02-OCT-1997; 97DE-1043671.
XX
XX (GVSE-) GVS GES ERWERB & VERWERTUNG LANDWIRTSCHA.
XX
XX Saal B, Wricke G;
XX
XX WPI; 1999-245522/21.
XX
XX Microsatellite markers derived from the genome of rye, useful for
PT genetic mapping as markers of monogenic or polygenic traits
XX
XX Claim 6; Page 16; 28pp; German.
XX
XX This invention describes Secale cereale microsatellite markers based on
CC hypervariable genomic segments of Secale cereale and plants of the
CC tribes Triticeae and Poaceae. The microsatellite markers comprise a simple
CC sequence repeat (SSR) marker as sequence tag site (STS), defined by two
CC specific S. cereale defined primers, of mean length 18-26 bases and
CC flanking the microsatellite sequence (MSS). Such markers are useful for
CC genetic analysis of rye, triticale and other species of the tribes
CC Triticeae and Poaceae, e.g. for DNA fingerprinting; identification of
CC varieties; detecting self or cross fertilization; studying similarity
CC and relatedness; characterization of cytological lines, or generally any
CC sort of gene mapping. Particularly, they are useful for genetic mapping
CC and marking of mono- or poly-genic traits, selection and evaluation of
CC varietal purity or checking culture stages (particularly in hybrid
CC culture methods), purity of propagative materials, success of
CC self-fertilization and required ratio of components in populations and
CC hybrids. AAX36902-X36965 represent PCR primers used in the method of the
CC invention.
XX
XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
SQ
Query Match 60.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 8
AAZ36173
ID AAX36173 standard; DNA; 24 BP.
XX
XX
AC AAX36173;
XX
XX 15-JUL-1999 (first entry)
XX
XX PCR primer used to amplify a fragment of ICAM-6 nucleic acid.
DE Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;
KW intercellular adhesion; inflammatory process; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9920762-A1.
XX
XX 29-APR-1999.
XX

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PP 22-OCT-1998; 98WO-US22442.
 XX
 PR 22-OCT-1997; 97US-0955661.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Loughney K, Staunton DE, Vazeau R;
 XX WPI; 1999-288308/24.
 XX
 XX New isolated intercellular adhesion molecule-6 used for, e.g.
 PT diagnosis of inflammatory processes
 PT
 XX Example 15; Page 53; 102pp; English.
 XX
 XX The specification describes an intercellular adhesion molecule
 CC (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides
 CC can be used for drug screening and developing products for therapy
 CC involving intercellular adhesion, e.g. in inflammatory processes.
 CC The products can also be used for detection, diagnosis and the
 CC production of transgenic animals. PCR primers AAX36170-73 were used
 CC in the course of the invention.
 XX
 XX Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
 SQ

Query Match 60.0%; Score 12; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCA 13
 DB 1 TGACAGAGCCCA 12

RESULT 9

AAI74547/c
 ID AAI74547 standard; DNA; 43 BP.

XX AC AAI74547;
 XX
 DT 09-NOV-2001 (first entry)
 XX

DE Human silent SNP containing nucleic acid SEQ:1488.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX

OS Homo sapiens.

XX WO200140521-A2.

PN 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32758.

XX 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

XX Claim 1; Page 509; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of the
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

SQ Sequence 43 BP; 10 A; 14 C; 6 G; 13 T; 0 other;

Query Match 60.0%; Score 12; DB 22; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 14

DB 28 GACAGAGCCCA 17

RESULT 10

AAI74549/c

ID AAI74549 standard; DNA; 46 BP.

XX AC AAI74549;

XX 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:1490.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX WO200140521-A2.

PN 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32758.

XX 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

XX Claim 1; Page 509; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.
 XX
 SQ Sequence 46 BP; 10 A; 15 C; 6 G; 15 T; 0 other;

Query Match 60.0%; Score 12; DB 22; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
 |||||
 Db 28 GACAGAGCCCAA 17

RESULT 11
 AAA40237
 ID AAA40237 standard; DNA; 50 BP.

XX AAA40237;

XX 02-NOV-2000 (first entry)

XX Construct pC2-m9#518 primer P-CC(4).

XX Factor VIII; light chain; LRP; gene therapy; antihemophilic; blood;
 KW low density lipoprotein receptor-related protein; coagulation disorder;
 KW thrombotic system; fibrinolytic system; primer; ss.

XX Unidentified.

XX WO200028021-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-AF00272.

XX 10-NOV-1998; 98AT-0001872.

XX (BAXT) BAXTER AG.

XX Lenting PJ, Van Mourik JA, Mertens K, Pannekoek H, Turecek P;
 PI Schwarz H, Scheiflinger F;

XX WPI; 2000-376538/32.

XX New modified form of factor VIII, useful for treating hemophilia, has
 PT altered binding to low density lipoprotein-related protein, resulting
 PT in extended in vivo half-life

XX Example XI; Page 35; 57pp; German.

XX This invention describes a novel factor VIII polypeptide (I) with factor
 CC VIII:C activity which has a modification in at least one of the A3, C1
 CC and/or C2 domains of the light chain that modifies binding affinity to
 CC low density lipoprotein receptor-related protein (LRP). Independent
 CC claims are also included for the following: (1) DNA (II) that encodes
 CC (1); (2) an expression vector containing (II); (3) transformed cells and
 CC their descendants containing (II); (4) recombinant production of (I) by
 CC culturing cells of (C); and (5) pharmaceutical composition containing a
 CC factor VIII molecule (Ia) with factor VIII:C activity plus an LRP
 CC antagonist (III). The products of the invention have antihemophilic
 CC activity. (I) has reduced affinity for LRP, a receptor involved in
 CC clearance of factor VIII from the blood. (I), optionally formulated with
 CC an antagonist of LRP, is used for treatment of coagulation disorders,
 CC specifically hemophilia A. It may also be used to treat subjects with

CC disorders of the thrombotic or fibrinolytic systems, e.g. before,
 CC during or after surgery. Nucleic acid that encodes (I) can be used
 CC similarly in gene therapy. The light chain modifications reduce clearance
 CC of factor VIII protein from the blood, resulting in longer in vivo
 CC half-life (particularly at least 90% greater than wild type) and
 CC increased stability, in vivo or in vitro. The modifications do not
 CC adversely affect procoagulant activity. This sequence represents a primer
 CC used in the construction of the plasmid pC2-m9#518 which contains the
 CC Factor VIII light chain C2 region which is described in the method of the
 CC invention.

XX Sequence 50 BP; 11 A; 16 C; 15 G; 8 T; 0 other;

Query Match 60.0%; Score 12; DB 21; Length 50;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCT 18
 |||||
 Db 31 GAGCCCAACTCT 42

RESULT 12
 ABF03254/c
 ID ABF03254 standard; DNA; 13 BP.

XX ABF03254;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 103251 for detecting SNP TSC0025831.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 103251; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABH99989 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 other;

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Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 12 GCCCAACTCTT 2

RESULT 13
ABF03255
ID ABF03255 standard; DNA; 13 BP.
XX
AC ABF03255;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 103252 for detecting SNP TSC0025831.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
XX
Claim 1; SEQ ID 103252; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
XX
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
XX
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 other;

Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 2 GCCCAACTCTT 12

RESULT 14
ABH33140/c
ID ABH33140 standard; DNA; 13 BP.
XX

```

```

AC ABH33140;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 233117 for detecting SNP TSC0000563.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
XX
Claim 1; SEQ ID 233117; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
XX
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
XX
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 other;

Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCCACTCTTC 20
Db 13 CCCCACTCTTC 3

RESULT 15
ABH33141
ID ABH33141 standard; DNA; 13 BP.
XX
AC ABH33141;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 233118 for detecting SNP TSC0000563.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

```

XX 18-OCT-2001.
 XX PD
 XX PF 06-APR-2001; 2001WO-1B00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX PS Claim 1; SEQ ID 233118; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 other;

Query Match 55.0%; Score 11; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CCCAACTCTTC 20
 Db 1 CCCAACTCTTC 11

Search completed: June 23, 2003, 05:43:36
 Job time : 133.216 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGCCCACTCTTC 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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2: em_esthum:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	60.0	46	17	AZ379320
C 2	11	55.0	21	17	AZ781467
C 3	11	55.0	22	17	AZ393281
C 4	11	55.0	24	17	AZ309564
C 5	11	55.0	47	10	BES36289
C 6	10	50.0	22	9	AI687266

7	10	50.0	23	17	AZ331549
8	10	50.0	25	9	AI647975
C 9	10	50.0	28	17	AZ939438
C 10	10	50.0	29	17	AZ412468
C 11	10	50.0	30	17	AZ310102
C 12	10	50.0	37	9	AI572041
C 13	10	50.0	37	12	BG423450
C 14	10	50.0	37	13	BI765481
C 15	10	50.0	37	13	BJ063841
C 16	10	50.0	38	14	H45829
C 17	10	50.0	39	17	AZ773780
C 18	10	50.0	42	17	AZ616105
C 19	10	50.0	43	9	AI091574
C 20	10	50.0	44	17	AZ309736
C 21	10	50.0	45	9	AI309096
C 22	10	50.0	45	17	AZ653181
C 23	10	50.0	50	9	AUI04061
C 24	10	50.0	50	9	AUI06667
C 25	10	50.0	50	9	AUI06839
C 26	9	45.0	19	17	AZ775541
C 27	9	45.0	21	17	AZ816100
C 28	9	45.0	23	17	AZ466178
C 29	9	45.0	24	17	AZ852116
C 30	9	45.0	25	17	AZ829708
C 31	9	45.0	28	9	AI756191
C 32	9	45.0	28	17	AZ990764
C 33	9	45.0	28	17	BH848229
C 34	9	45.0	29	17	AZ804299
C 35	9	45.0	30	17	AZ458346
C 36	9	45.0	30	17	AZ486857
C 37	9	45.0	31	17	AZ856886
C 38	9	45.0	32	10	AV962684
C 39	9	45.0	32	14	N72637
C 40	9	45.0	33	17	AZ424922
C 41	9	45.0	33	17	BH790221
C 42	9	45.0	34	9	AA798808
C 43	9	45.0	34	14	T89869
C 44	9	45.0	35	9	AI801185
C 45	9	45.0	36	13	BI549792

ALIGNMENTS

RESULT 1
AZ379320/c
LOCUS AZ379320 46 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0134F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0134F22 F, DNA sequence.
ACCESSION AZ379320
VERSION AZ379320.1 GI:10493020
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 46)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0134 row: P column: 22
 Seq primer: CATTGTAAACACAGCCAGT
 Class: plasmid ends
 High quality sequence stop: 46.

FEATURES

source

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1. .46
  Location/Qualifiers
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M00134P22"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
```

```

BASE COUNT      5 a      6 c      16 g      19 t
ORIGIN
Query Match      60.0%; Score 12; DB 17; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 ACAGAGCCCAAC 15
      |||||
Db      19 ACAGAGCCCAAC 8
  
```

RESULT 2

```

AZ781467/c
LOCUS      AZ781467      21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION      2M0019F23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0019F23 R, DNA sequence.
ACCESSION      AZ781467
VERSION      AZ781467.1 GI:12914189
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
  
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Plate: 0019 row: F column: 23
 Seq primer: CACACGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

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1. .21
  Location/Qualifiers
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0019F23"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
```

```

BASE COUNT      2 a      2 c      12 g      5 t
ORIGIN
Query Match      55.0%; Score 11; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 ACAGAGCCCAAC 14
      |||||
Db      11 ACAGAGCCCAAC 1
  
```

RESULT 3

```

AZ393281/c
LOCUS      AZ393281      22 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      1M0156H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0156H13 F, DNA sequence.
ACCESSION      AZ393281
VERSION      AZ393281.1 GI:10508353
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
  
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Plate: 0156 row: H column: 13
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0156H13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 4 a 4 c 7 g 7 t

Query Match 55.0%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCCA 14
 |||||
 Db 21 ACAGAGCCCCA 11

RESULT 4
 AZ309564
 LOCUS 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0016509F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016509 F, DNA sequence.

ACCESSION AZ309564
 VERSION AZ309564.1 GI:10350859
 KEYWORDS GSS.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: E column: 09
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

source

1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0016E09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 6 a 4 c 10 g 4 t

Query Match 55.0%; Score 11; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
 |||||
 Db 8 GACAGAGCCCA 18

RESULT 5
 BE536289/C
 LOCUS BE536289 47 bp mRNA linear EST 09-AUG-2000
 DEFINITION 601062681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:344989 5', mRNA sequence.

ACCESSION BE536289
 VERSION BE536289.1 GI:9764934
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 47)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM8425 row: a column: 22
 High quality sequence stop: 47.
 Location/Qualifiers
 1..47

FEATURES

source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3448989"
/clone_lib="NIH MGC_10"
/cell_line="MGC36"
/lab_host="DH108"
/site="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 Kb. Library prepared by Life
Technologies."
BASE COUNT      6 a      21 c      10 g      10 t
ORIGIN
Query Match      55.0%; Score 11; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3      GACAGAGCCCA 13
Db      34      GACAGAGCCCA 24
|||||
RESULT 6
AI687266/c
LOCUS
DEFINITION
tp94d10.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2206963 3'
similar to SW:DXS8 HUMAN P98175 DXS8237E PROTEIN ;contains element
MER22 repetitive element ; mRNA sequence.
ACCESSION
AI687266
VERSION
AI687266.1 GI:4898560
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 22)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1074 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..22
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2206963"
/clone_lib="NCI CGAP Ut3"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH108"
/site="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 Kb. Life Technologies catalog #:
11541-018"
BASE COUNT      0 a      2 c      13 g      7 t
ORIGIN
Query Match      50.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="UUCG1M0059K02"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      11 c      0 g      6 t
ORIGIN
Query Match      50.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5      CAGAGCCCAA 14
Db      12      CAGAGCCCAA 3
|||||
RESULT 7
AZ331549
LOCUS
DEFINITION
IM0059K02R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0059K02 R, DNA sequence.
ACCESSION
AZ331549
VERSION
AZ331549.1 GI:10394350
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: K column: 02
Seq primer: CACACGAGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1..23
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0059K02"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      11 c      0 g      6 t
ORIGIN
Query Match      50.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTC 20
 |||||
 Db 12 CCAACTCTTC 21

RESULT 8
 AI647975/c
 LOCUS
 DEFINITION
 uk38f04.x1 Sugano mouse kidney mkoa Mus musculus cDNA clone
 IMAGE:1971295.3' similar to SW:WS3_HUMAN O00399 WS-3 PROTEIN. ;
 mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AI647975.1 GI:4726653
 house mouse.
 Mus musculus

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TEL: 801 585 5606
 FAX: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0198 row: 1 column: 21
 Seq primer: CTTGTAAACGACGCGCAGT
 Class: plasmid ends

High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="Sugano mouse kidney mkoa"
 /sex="female"
 /dev_stage="adult"
 /lab_host="PH108"
 /note="Organ: kidney; Vector: pME18S-FL3; Site1: DralII
 (CACTGTGG); Site 2: DralII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DralII adaptor [CTGTGCGCTACTGG], digested
 and cloned into distinct DralII sites of the pME18S-FL3
 vector 15' site CACTGTGG, 3' site CACCATGTG. XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTCTCTTAAAGCTGG and 3' end
 primer CCACCTGCAGCTCAGACAA."

BASE COUNT 3 a 5 c 7 g 10 t
 ORIGIN

Query Match 50.0%; Score 10; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCA 13
 |||||
 Db 10 ACAGAGCCCA 1

RESULT 9
 AZ939438/c
 LOCUS
 DEFINITION
 2M0198121F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0198121 F, DNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AZ939438.1 GI:13800110
 house mouse.
 Mus musculus

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TEL: 801 585 5606
 FAX: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0198 row: 1 column: 21
 Seq primer: CTTGTAAACGACGCGCAGT
 Class: plasmid ends

High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /sex="female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 10 a 7 c 5 g 6 t
 ORIGIN

Query Match 50.0%; Score 10; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACT 16
 |||||
 Db 25 GAGCCCAACT 16

RESULT 10
 AZ412468/c
 LOCUS
 DEFINITION 29 bp DNA linear GSS 03-OCT-2000
 clone UUGC1M0185M20 R, DNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Insert Length: 10000 Std Error: 0.00
 Plate: 0185 row: M column: 20
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source
 1..29
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0185M20"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse, DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 3 c 13 g 10 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGCCCAACTC 17
 |||||
 Db 15 AGCCCAACTC 6

RESULT 11
 AZ310102/c
 LOCUS
 DEFINITION 30 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0018D24 R, DNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Insert Length: 10000 Std Error: 0.00
 Plate: 0018 row: D column: 24
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 30.

FEATURES
 source
 1..30
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0018D24"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse, DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 2 a 14 c 5 g 9 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTGACAGAGC 10
Db 24 CTGACAGAGC 15

RESULT 12
LOCUS AI572041
DEFINITION tr72h02.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2223891 3'
similar to SW:PRCF HUMAN P40306 PROTEASOME COMPONENT MECL-1
PRECURSOR : mRNA sequence.
ACCESSION AI572041
VERSION AI572041.1 GI:4535415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Cloned through the NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 770 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No. Location/Qualifiers
1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2223891"
/clone_lib="NCI CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life technologies catalog #:
11548-013"
7 a 9 c 14 g 5 t

BASE COUNT 9 a 9 c 14 g 5 t
ORIGIN
Query Match 50.0%; Score 10; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 5 CAGAGCCCAA 14
Db 13 CAGAGCCCAA 22

RESULT 13
LOCUS BG423450
DEFINITION 602449304F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4587696 5',
mRNA sequence.
ACCESSION BG423450
VERSION BG423450.1 GI:13329956
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)

QY 37 bp mRNA linear EST 14-MAR-2001
LOCUS BG423450
DEFINITION 602449304F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4587696 5',
mRNA sequence.
ACCESSION BG423450
VERSION BG423450.1 GI:13329956
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1476 row: 1 column: 12
High quality sequence stop: 37.
Location/Qualifiers
1. .37
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/db_xref="taxon:9606"

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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DClD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMI318 row: h column: 01
High quality sequence stop: 37.
Location/Qualifiers
1. .37
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/db_xref="taxon:9606"
/clone="IMAGE:4587696"
/clone_lib="NIH MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
7 a 11 c 12 g 7 t

BASE COUNT 7 a 11 c 12 g 7 t
ORIGIN
Query Match 50.0%; Score 10; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 CTGACAGAGC 10
Db 20 CTGACAGAGC 29

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DEFINITION 603050546F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190683 5',
mRNA sequence.
ACCESSION BI765481
VERSION BI765481.1 GI:15757059
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1476 row: 1 column: 12
High quality sequence stop: 37.
Location/Qualifiers
1. .37
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/db_xref="taxon:9606"

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Db 24 CCAACTCTTC 33
 Search completed: June 23, 2003, 10:10:21
 Job time : 1033.31 secs

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 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dr primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH MGC Library."

BASE COUNT 7 a 6 c 22 g 2 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 13; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCT 18
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 Db 21 GCCCAACTCT 12

RESULT 15
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 LOCUS
 DEFINITION BJ063841 NIBB Mochii normalized Xenopus tailbud library Xenopus
 laevis cDNA clone XL077114 5', mRNA sequence.
 ACCESSION BJ063841
 VERSION BJ063841.1 GI:17471031
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM
 Xenopus laevis
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tahini@genes.nig.ac.jp.
 Location/Qualifiers

FEATURES
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 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="XL077114"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /note="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dr primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library is subtracted
 and was constructed by N. Garrett and A.M. Zorn,
 (Wellcome/CRC Institute)."
 5 a 15 c 3 g 13 t 1 others

BASE COUNT 5 a 15 c 3 g 13 t 1 others
 ORIGIN
 Query Match 50.0%; Score 10; DB 13; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 11 CCAACTCTTC 20

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

Searched: 441362 seqs, 153338391 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	14	70.0	26	3	US-08-974-180-33
5	12.8	64.0	30	4	US-08-339-214-100
6	12.6	63.0	20	4	US-09-657-452A-168
7	12.6	63.0	35	4	US-09-270-542-130
8	12.6	63.0	41	1	US-08-305-700-1
9	12.6	63.0	41	1	US-08-528-122-1
10	12.6	63.0	41	5	PCT-US95-11720-1
11	12.4	62.0	15	1	US-08-311-486C-658
12	12.4	62.0	20	3	US-09-166-186-135
13	12.4	62.0	20	4	US-09-313-932-135
14	12.4	62.0	40	4	US-09-410-903-74
15	12.4	62.0	45	1	US-08-171-389-10
16	12.4	62.0	45	1	US-08-123-936-10
17	12.4	62.0	45	2	US-08-475-228A-10
18	12.4	62.0	45	3	US-08-482-080A-10
19	12.4	62.0	45	4	US-09-354-947-10
20	12.4	62.0	45	5	PCT-US93-12388-10
21	12.2	61.0	20	1	US-08-469-802B-21
22	12.2	61.0	20	2	US-08-267-803B-39
23	12.2	61.0	20	4	US-09-467-642-63
24	12.2	61.0	31	4	US-09-648-040-1
25	12	60.0	21	1	US-08-031-143B-29
26	12	60.0	21	5	PCT-US94-02891-29
27	12	60.0	30	1	US-08-484-557C-46

c 28	12	60.0	30	1	US-08-487-426B-46	Sequence 46, Appl
c 29	12	60.0	30	2	US-08-487-720A-46	Sequence 46, Appl
c 30	12	60.0	37	1	US-08-653-740-30	Sequence 30, Appl
c 31	12	60.0	37	2	US-09-073-594-30	Sequence 30, Appl
c 32	12	60.0	37	3	US-09-275-925-30	Sequence 30, Appl
c 33	12	60.0	40	3	US-08-831-132-16	Sequence 16, Appl
c 34	12	60.0	40	4	US-09-416-150-16	Sequence 16, Appl
c 35	12	60.0	48	2	US-08-448-418-56	Sequence 56, Appl
c 36	11.8	59.0	20	2	US-08-726-012B-12	Sequence 12, Appl
c 37	11.8	59.0	20	4	US-09-487-445-141	Sequence 141, Appl
c 38	11.8	59.0	27	1	US-08-196-538-8	Sequence 8, Appl
c 39	11.8	59.0	39	3	US-08-630-820-3	Sequence 3, Appl
c 40	11.8	59.0	39	4	US-08-706-945D-24	Sequence 24, Appl
c 41	11.8	59.0	42	4	US-09-142-956B-8	Sequence 8, Appl
c 42	11.8	59.0	42	4	US-09-142-956B-9	Sequence 9, Appl
c 43	11.6	58.0	20	1	US-08-222-177A-155	Sequence 155, Appl
c 44	11.6	58.0	20	3	US-08-338-579A-49	Sequence 49, Appl
c 45	11.6	58.0	20	4	US-09-487-368A-141	Sequence 141, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20
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US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-5

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20
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RESULT 3

US-09-051-363-23/c
; Sequence 23, Application US/09051363
; Patent No. 6270993
; GENERAL INFORMATION:
; APPLICANT: Shibuya, Masabumi
; APPLICANT: Okamoto, Masaji
; APPLICANT: Niwa, Mikio
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Asano, Makoto
; APPLICANT: Segawa, Toshiaki
; TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; --- ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,363
; FILING DATE: 07-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/02906
; FILING DATE: 07-OCT-1996
; APPLICATION NUMBER: 8/211892 JP
; FILING DATE: 23-JUL-1996
; APPLICATION NUMBER: 7/296476 JP
; FILING DATE: 07-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic DNA
; US-09-051-363-23

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Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACAGAGCCCAACTCTT 19
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Db 24 ACAGAGCCCAACTCTT 9
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RESULT 4

US-08-974-180-33/c
; Sequence 33, Application US/08974180
; Patent No. 6025194
; GENERAL INFORMATION:
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Methods for Modulating and Identifying
; TITLE OF INVENTION: Cellular Senescence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Geron Corporation
; STREET: 230 Constitution Drive
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,180
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaster, Kevin R.

REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 206
TELEPHONE: (650) 473-7779
TELEFAX: (650) 473-8654
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..26
OTHER INFORMATION: /note= "primer htr S328"

US-08-974-180-33

Query Match 70.0%; Score 14; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 CTGACAGAGCCCAA 1

RESULT 5

US-08-339-214-100
Sequence 100, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
TITLE OF INVENTION: Encoding the Same
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolsach & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "sense primer 19"
ANTI-SENSE: NO

US-08-339-214-100

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Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTTC 20
Db 10 CAAAGCCCAAGCTCTTC 25

RESULT 6

US-09-657-452A-168
Sequence 168, Application US/09657452A
Patent No. 6426188
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION
FILE REFERENCE: RTS-0125
CURRENT APPLICATION NUMBER: US/09/657,452A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 168
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-452A-168

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Best Local Similarity 78.9%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 1 TGCCAGAGTCCAGCTCATC 19

RESULT 7

US-09-270-542-130
Sequence 130, Application US/09270542
Patent No. 632976
GENERAL INFORMATION:
APPLICANT: Altman, Timothy
APPLICANT: Scott, James
APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/09/270,542
CURRENT FILING DATE: 1999-03-17
EARLIER APPLICATION NUMBER: 09/221,222
EARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 130
LENGTH: 35
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-270-542-130

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Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 10 TCAAAGAGTCCCAAGCTCTTC 28

RESULT 8

US-08-305-700-1
Sequence 1, Application US/08305700

Patent No. 5541087
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOFUSINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,700
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-305-700-1

Query Match 63.0%; Score 12.6; DB 1; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
DB 10 TAAGCGAGCCCAAACTCTC 28

RESULT 9
US-08-528-122-1
Sequence 1, Application US/08528122
Patent No. 5726044
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOFUSINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-528-122-1

Query Match 63.0%; Score 12.6; DB 1; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
DB 10 TAAGCGAGCCCAAACTCTC 28

RESULT 10
PCT-US95-11720-1
Sequence 1, Application PC/IUS9511720
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOFUSINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11720
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-11720-1

Query Match 63.0%; Score 12.6; DB 5; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACGAGCCCAACTCTTC 20
| | | | | | | | | |
Db 10 TAAGCGAGCCCAACTCTTC 28

RESULT 11

US-08-311-486C-658
; Sequence 658, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Kisich
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggan
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: TNF-
; NUMBER OF SEQUENCES: 1157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,486C
; FILING DATE: September 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 658:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-486C-658

Query Match 62.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 5.8e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
| | | | | | | | | |
Db 2 CAGAGCCCAACUCU 15

RESULT 12

US-09-166-186-135/c
; Sequence 135, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-186-135

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 6.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
| | | | | | | | | |
Db 17 CAGAGTCCAACCTCT 4

RESULT 13

US-09-313-932-135/c
; Sequence 135, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-313-932-135

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 6.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
| | | | | | | | | |
Db 17 CAGAGTCCAACCTCT 4

RESULT 14

US-09-410-903-74/c
; Sequence 74, Application US/09410903
; Patent No. 6420113
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Biosite Diagnostics Inc.
; TITLE OF INVENTION: Chimeric Polyclonal Antibodies
; FILE REFERENCE: 014907-002700US

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; CURRENT APPLICATION NUMBER: US/09/410,903
; CURRENT FILING DATE: 1999-10-02
; PRIOR APPLICATION NUMBER: US 08/832,985
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: US 08/835,159
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: WO PCT/US98/06704
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide 3' PCR primer 876
US-09-410-903-74

Query Match          62.0%; Score 12.4; DB 4; Length 43;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTCT 18
      |||||
Db      32 CAGAGCCCAACTCT 19

RESULT 15
US-08-171-389-10
; Sequence 10, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,389
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; TYPE: DNA
; INDIVIDUAL ISOLATE: Human gene fragment for the
; INDIVIDUAL ISOLATE: acetylcholine receptor gamma
US-08-171-389-10

Query Match          62.0%; Score 12.4; DB 1; Length 45;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTCT 18
      |||||
Db      32 CAGAGCCCAACTCT 45

Search completed: June 25, 2003, 00:24:37
Job time : 31.3586 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCAACTCTTC 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PTCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	19	9	US-10-093-958-22
2	13.6	68.0	28	9	US-10-151-320-25
3	13.6	68.0	28	9	US-10-152-363A-48
4	13.6	68.0	29	9	US-10-152-363A-41
5	13.6	68.0	29	9	US-10-152-363A-42
6	13.6	68.0	28	9	US-10-152-363A-16
7	13.4	67.0	21	9	US-09-909-567B-23
8	13.4	67.0	33	9	US-10-006-591-8
9	13.4	67.0	35	9	US-10-216-484-86
10	13.2	66.0	25	9	US-10-098-263B-39849
11	13.2	66.0	25	9	US-10-098-263B-57306
12	13.2	66.0	28	9	US-10-152-363A-46
13	13.2	66.0	30	9	US-10-152-363A-43
14	13.2	66.0	31	9	US-10-152-363A-44
15	13.2	66.0	30	9	US-09-874-503-31
16	13.2	66.0	50	9	US-10-000-157-31
17	13.2	66.0	50	9	US-09-747-259-31
18	13.2	66.0	50	9	US-09-908-821-31
19	12.8	64.0	25	9	US-10-098-263B-2034

20	12.8	64.0	36	9	US-10-008-063-39
21	12.8	64.0	36	10	US-09-375-924C-9
22	12.6	63.0	36	9	US-10-218-547-53
23	12.6	63.0	36	9	US-10-218-547-55
24	12.6	63.0	49	9	US-10-006-009-4
25	12.4	62.0	20	9	US-09-824-322B-135
26	12.4	62.0	31	9	US-09-288-971-6
27	12.4	62.0	31	9	US-09-288-971-10
28	12.4	62.0	31	10	US-09-801-274-1303
29	12.4	62.0	36	9	US-10-008-063-29
30	12.4	62.0	36	9	US-10-152-363A-19
31	12.4	62.0	43	9	US-09-453-234-27
32	12.4	62.0	43	9	US-10-193-960-74
33	12.2	61.0	17	9	US-09-930-423-1249
34	12.2	61.0	17	9	US-09-930-423-1614
35	12.2	61.0	18	10	US-09-969-373-1891
36	12.2	61.0	22	9	US-09-791-389-304
37	12.2	61.0	22	9	US-09-791-393-304
38	12.2	61.0	22	10	US-09-791-378-662
39	12.2	61.0	22	10	US-09-791-378-670
40	12.2	61.0	25	9	US-10-098-263B-47598
41	12.2	61.0	25	9	US-10-098-263B-65640
42	12.2	61.0	25	9	US-10-098-263B-112540
43	12.2	61.0	30	9	US-09-977-418-78
44	12.2	61.0	30	9	US-09-977-033A-78
45	12.2	61.0	31	9	US-10-217-914-1

ALIGNMENTS

RESULT 1
US-10-093-958-22
; Sequence 22, Application US/10093958
; Publication No. US2003004423A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
; TITLE OF INVENTION: Moiey
; FILE REFERENCE: LEX-016
; CURRENT APPLICATION NUMBER: US/10/093,958
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
Db 4 CAGAGCCCAACTCTTC 19

RESULT 2
US-10-151-320-25
; Sequence 25, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436

```

; CURRENT APPLICATION NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer used for PCR.
US-10-151-320-25

Query Match      68.0%; Score 13.6; DB 9; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
      ||| ||| ||| ||| ||| ||| |||
Db      1 CTGGCCAGCCCAACTCTTC 20

RESULT 3
US-10-152-363A-48
; Sequence 48, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-48

Query Match      68.0%; Score 13.6; DB 9; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
      ||| ||| ||| ||| ||| ||| |||
Db      4 CTCAGGAGCCCAACTCTTC 23

RESULT 4
US-10-152-363A-41/c
; Sequence 41, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: PCR primer.
US-10-152-363A-41

Query Match      68.0%; Score 13.6; DB 9; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
      ||| ||| ||| ||| ||| ||| |||
Db      21 CTCAGGAGCCCAACTCTTC 2

RESULT 5
US-10-152-363A-42
; Sequence 42, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-42

Query Match      68.0%; Score 13.6; DB 9; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
      ||| ||| ||| ||| ||| ||| |||
Db      9 CTCAGGAGCCCAACTCTTC 28

RESULT 6
US-10-152-363A-16/c
; Sequence 16, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-16

Query Match      68.0%; Score 13.6; DB 9; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
      ||| ||| ||| ||| ||| ||| |||

```


Db 39 CTGAAGGAGCCGAGATCTTC 20

RESULT 7

US-09-909-567B-23
; Sequence 23, Application US/09909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tanaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-909-567B-23

Query Match 67.0%; Score 13.4; DB 9; Length 21;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTT 19
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Db 2 CAGAGCCCAACTCTT 16
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RESULT 8

US-10-006-591-8/c
; Sequence 8, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GENES
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description for Artificial Sequence: primer
US-10-006-591-8

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Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTT 19
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RESULT 9

US-10-216-484-86
; Sequence 86, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tanaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 86
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain
; OTHER INFORMATION: chain
US-10-216-484-86

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Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 7 CAGAGCCCAACTCTT 21
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RESULT 10

US-10-098-263B-39849
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 39849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-39849

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 8 GACAGAGACCTATTCTTC 25
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RESULT 11

US-10-098-263B-57306/c
; Sequence 57306, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael

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;; PRIOR APPLICATION NUMBER: US 60/130,232
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;; PRIOR APPLICATION NUMBER: US 60/113,621
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;; PRIOR FILING DATE: 2001-05-10
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;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
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;; PRIOR FILING DATE: 1999-03-08
;; NUMBER OF SEQ ID NOS: 39
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;; TYPE: DNA
;; ORGANISM: Artificial Sequence

;; FEATURE:
;; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-874-503-31

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Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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5	18	90.0	24	9	US-08-521-634-15
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7	15.8	79.0	25	17	US-09-396-196G-124326
8	14.8	74.0	25	79	US-60-353-987-992959
9	14.4	72.0	19	1	PCT-US02-07011-22
10	14.4	72.0	19	39	US-10-093-958-22
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ALIGNMENTS

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RESULT 1
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; Sequence 6, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 16ab"
PCT-US97-23619-6

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
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; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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US-08-770-564A-6

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Best Local Similarity 100.0%; Pred. No. 22;
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RESULT 3
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Sequence 5, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..30
OTHER INFORMATION: /note= "oligo 16"
PCT-US97-23619-5
Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20
RESULT 4
US-08-770-564A-5
Sequence 5, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-5
Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20
RESULT 5
US-08-521-634-15/c
Sequence 15, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match 90.0%; Score 18; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
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DB 24 GACAGAGCCCAACTCTTC 7

RESULT 6

US-09-396-196F-124326
Sequence 124326, Application US/09396196F
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196F
CURRENT FILING DATE: 2001-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 124326
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196F-124326

Query Match 79.0%; Score 15.8; DB 17; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
DB 2 TGACAGAGCCCAAGTCTTC 20

RESULT 7

US-09-396-196G-124326
Sequence 124326, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 124326
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-124326

Query Match 79.0%; Score 15.8; DB 17; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
DB 2 TGACAGAGCCCAAGTCTTC 20

RESULT 8

US-60-353-987-992959
Sequence 992959, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 992959
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-353-987-992959

Query Match 74.0%; Score 14.8; DB 79; Length 25;
Best Local Similarity 88.9%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTT 19
|||||
DB 4 TGACAGAGCCCAACTCTT 21

RESULT 9

PCT-US02-07011-22
Sequence 22, Application PC/TUS0207011
GENERAL INFORMATION:
APPLICANT: Lexigen Pharmaceuticals Corp.
APPLICANT: Gillies, Stephen
APPLICANT: Way, Jeffrey
TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
TITLE OF INVENTION: Moieti
FILE REFERENCE: LEX-016PC
CURRENT APPLICATION NUMBER: PCT/US02/07011
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,096
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 19
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: forward primer for gamma 1 hinge region
PCT-US02-07011-22

Query Match 72.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
|||||
Db 4 CAGAGCCCAACTCTTC 19

RESULT 10
US-10-093-958-22
; Sequence 22, Application US/10093958
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Jeffrey, Way
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype A
; TITLE OF INVENTION: Moiety
; FILE REFERENCE: LEX-016
; CURRENT APPLICATION NUMBER: US/10/093,958
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 39; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
|||||
Db 4 CAGAGCCCAACTCTTC 19

RESULT 11
US-09-396-196F-9984/c
; Sequence 9984, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196F-9984

Query Match 71.0%; Score 14.2; DB 17; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
Db 20 TGCCAGAGCCCAACATC 2

RESULT 12
US-09-396-196G-9984/c
; Sequence 9984, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-9984

Query Match 71.0%; Score 14.2; DB 17; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
Db 20 TGCCAGAGCCCAACATC 2

RESULT 13
US-09-660-220-102700
; Sequence 102700, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U73824
US-09-660-220-102700

Query Match 71.0%; Score 14.2; DB 26; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTT 19
|||||
Db 5 CTGACGAGAGCAGCAACTCTT 23

RESULT 14
US-09-954-427-80617
; Sequence 80617, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80617
; LENGTH: 25
; TYPE: DNA

Search completed: June 25, 2003, 06:20:24
Job time : 1698.67 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-6
Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTTTC 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:*
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13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	23	1	PCT-US03-04088-522
C 2	19	95.0	21	1	PCT-US03-04088-522
C 3	19	95.0	21	1	PCT-US03-04088-544
C 4	19	95.0	21	1	PCT-US03-04088-548
C 5	19	95.0	21	1	PCT-US03-04088-552
C 6	19	95.0	21	1	PCT-US03-04088-556
C 7	19	95.0	21	1	PCT-US03-04088-560
C 8	18	90.0	19	1	PCT-US03-04088-23
C 9	18	90.0	19	1	PCT-US03-04088-287
C 10	15.8	79.0	25	12	US-60-427-808-503841
C 11	14.8	74.0	25	9	US-10-355-577-992959
C 12	14.8	74.0	25	12	US-60-427-808-449334
C 13	14.8	74.0	25	12	US-60-427-836-142384
C 14	14.8	74.0	25	12	US-60-427-836-160311
C 15	14.4	72.0	25	12	US-60-427-836-166946
C 16	14.4	72.0	25	12	US-60-427-836-359518
C 17	14.2	71.0	25	6	US-09-660-222-102700
C 18	14.2	71.0	25	9	US-10-355-577-592670
C 19	14.2	71.0	25	9	US-10-355-577-736046
C 20	14.2	71.0	25	9	US-10-355-577-870013

C 21	14.2	71.0	25	12	US-60-427-808-420907	Sequence 420907,
C 22	14.2	71.0	25	12	US-60-427-808-423385	Sequence 423385,
C 23	14.2	71.0	25	12	US-60-427-808-467623	Sequence 467623,
C 24	14.2	71.0	25	12	US-60-427-808-503840	Sequence 503840,
C 25	14.2	71.0	25	12	US-60-427-808-764602	Sequence 764602,
C 26	14.2	71.0	47	9	US-10-349-143-3806	Sequence 3806, Ap
C 27	14	70.0	25	12	US-60-427-808-47221	Sequence 47221, A
C 28	14	70.0	25	12	US-60-427-808-699316	Sequence 699316,
C 29	14	70.0	25	12	US-60-427-836-529892	Sequence 529892,
C 30	13.8	69.0	20	10	US-10-289-762-5017	Sequence 5017, Ap
C 31	13.8	69.0	25	6	US-09-660-222-66821	Sequence 66821, A
C 32	13.8	69.0	25	6	US-09-660-222-66822	Sequence 66822, A
C 33	13.8	69.0	25	6	US-09-660-222-66827	Sequence 66827, A
C 34	13.8	69.0	25	7	US-09-953-570-97309	Sequence 97309, A
C 35	13.8	69.0	25	9	US-10-355-577-738193	Sequence 738193,
C 36	13.8	69.0	25	12	US-60-427-808-99506	Sequence 99506, A
C 37	13.8	69.0	25	12	US-60-427-808-104960	Sequence 104960,
C 38	13.8	69.0	25	12	US-60-427-808-263712	Sequence 263712,
C 39	13.8	69.0	25	12	US-60-427-808-317845	Sequence 317845,
C 40	13.8	69.0	25	12	US-60-427-808-461772	Sequence 461772,
C 41	13.8	69.0	25	12	US-60-427-808-589800	Sequence 589800,
C 42	13.8	69.0	25	12	US-60-427-836-258	Sequence 258, App
C 43	13.8	69.0	25	12	US-60-427-836-78476	Sequence 78476, A
C 44	13.8	69.0	25	12	US-60-427-836-316556	Sequence 316556,
C 45	13.6	68.0	23	10	US-10-372-730-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 100.0%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGACAGAGCCCAACTCTTC 20
Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
PCT-US03-04088-540/c
; Sequence 540, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 540
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-544

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
PCT-US03-04088-548/c
; Sequence 548, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 548
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
```

```
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAACTCTTC 20
      |||||
Db      19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 5
PCT-US03-04088-552
Sequence 552, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 552
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAACTCTTC 20
      :|||||
Db      1 UGACAGAGCCCAACUCUUC 19
```

```
RESULT 6
PCT-US03-04088-556/c
Sequence 556, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 556
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(6)
OTHER INFORMATION: 2'-deoxy
```

NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-556

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTC 20
DB 19 TGACAGAGCCCACTCTTC 1

RESULT 7
PCT-US03-04088-560
Sequence 560, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTC 20
DB 1 UGACAGAGCCCACTCTTC 19

RESULT 8
PCT-US03-04088-23/c
Sequence 23, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20

PCT-US03-04088-287
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-23

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCT 18
Db 18 CTGACAGAGCCCAACTCT 1

RESULT 9
PCT-US03-04088-287
; Sequence 287, Application PC/ITUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 287
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-287

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 34;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCT 18
Db 2 CUGACAGAGCCCAACUCU 19
RESULT 10
US-60-427-808-503841
; Sequence 503841, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 503841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-503841

Query Match 79.0%; Score 15.8; DB 12; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACAGAGCCCAACTCTC 20
Db 6 TGACAGAGCCCAAGTCCTC 24

RESULT 11
US-10-355-577-992959
; Sequence 992959, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 992959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-992959

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACAGAGCCCAACTCTT 19
Db 4 TGACAGAGCCCAACTCTT 21

RESULT 12
US-60-427-808-449334
; Sequence 449334, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 449334
; LENGTH: 25
; TYPE: DNA

```
; ORGANISM: Mus musculus
US-60-427-808-449334

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GACAGAGCCCAACTCTTC 20
        ||||| ||||| |||||
Db       1 GACAGTGTCCAACTCTTC 18

RESULT 13
US-60-427-836-142384
; Sequence 142384, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 142384
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-142384

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GACAGAGCCCAACTCTTC 20
        ||||| ||||| |||||
Db       7 GACTGAGCCCACTCTTC 24

RESULT 14
US-60-427-836-603511/c
; Sequence 603511, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 603511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-603511

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GACAGAGCCCAACTCTTC 20
        ||||| ||||| |||||
Db      19 GACAGAGACCAAGTCTTC 2

RESULT 15
US-60-427-836-166946/c
; Sequence 166946, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
;

; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-166946

Query Match          72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACT 16
        ||||| ||||| |||||
Db      16 CTGACAGTGCCTCAACT 1

Search completed: June 26, 2003, 04:15:15
Job time : 479.077 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
 Run on: June 23, 2003, 01:05:28 ; Search time 348.884 Seconds
 (without alignments)
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Title: US-08-770-564A-5
 Perfect score: 30
 Sequence: 1 CTGACAGACCCCAACTCTTCGCGTGGCAG 30

Scoring table: OLIGO NUC
 Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
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Minimum DB seq length: 0
 Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

1: gb.ba.*
 2: gb.htg.*
 3: gb.in.*
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 6: gb.pat.*
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 8: gb.pl.*
 9: gb.pr.*
 10: gb.ro.*
 11: gb.sts.*
 12: gb.sy.*
 13: gb.un.*
 14: gb.vi.*
 15: em.ba.*
 16: em.fun.*
 17: em.hum.*
 18: em.in.*
 19: em.mu.*
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 23: em.pat.*
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 25: em.pl.*
 26: em.ro.*
 27: em.sts.*
 28: em.un.*
 29: em.vi.*
 30: em.htg.hum.*
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 32: em.htg.other.*
 33: em.htg.mus.*
 34: em.htg.pln.*
 35: em.htg.rod.*
 36: em.htg.man.*
 37: em.htg.vrt.*
 38: em.sy.*
 39: em.htgo.hum.*
 40: em.htgo.mus.*
 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	30	6	AR063829	AR063829 Sequence
2	20	66.7	20	6	AR063830	AR063830 Sequence
3	20	66.7	20	6	AR063831	AR063831 Sequence
4	13	43.3	46	6	I28704	I28704 Sequence 7
5	12	40.0	20	12	AB069038	AB069038 Synthetic
6	12	40.0	26	6	AX109246	AX109246 Sequence
7	12	40.0	28	9	S72525	S72525 TCR V gamma
8	12	40.0	30	9	HSTCRGV33	X69253 H.sapiens m
9	12	40.0	43	6	AX158160	AX158160 Sequence
10	12	40.0	46	6	AX158162	AX158162 Sequence
11	12	40.0	50	6	AX024597	AX024597 Sequence
12	11	36.7	12	6	AI4857	AI4857 Nucleotide
13	11	36.7	15	6	AR056247	AR056247 Sequence
14	11	36.7	15	6	AR114005	AR114005 Sequence
15	11	36.7	18	6	A32455	A32455 Synthetic p
16	11	36.7	18	6	A32726	A32726 Synthetic d
17	11	36.7	18	6	I19611	I19611 Sequence 12
18	11	36.7	18	6	I84271	I84271 Sequence 42
19	11	36.7	20	6	A09892	A09892 Oligonucleo
20	11	36.7	20	6	A09923	A09923 Probe. 1/19
21	11	36.7	20	6	AI4859	AI4859 Nucleotide
22	11	36.7	20	6	A30766	A30766 Artificial
23	11	36.7	20	6	AR002212	AR002212 Sequence
24	11	36.7	20	6	E05218	E05218 Probe for g
25	11	36.7	20	6	E16501	E16501 PCR primer
26	11	36.7	20	12	AB069392	AB069392 Synthetic
27	11	36.7	21	6	A37934	A37934 Sequence 12
28	11	36.7	21	6	AR129457	AR129457 Sequence
29	11	36.7	21	6	AX110621	AX110621 Sequence
30	11	36.7	22	6	AX110619	AX110619 Sequence
31	11	36.7	24	6	A09925	A09925 Probe. 1/19
32	11	36.7	24	6	AR171201	AR171201 Sequence
33	11	36.7	24	6	AX068559	AX068559 Sequence
34	11	36.7	24	6	AX445639	AX445639 Sequence
35	11	36.7	24	6	AX445836	AX445836 Sequence
36	11	36.7	25	6	AX115384	AX115384 Sequence
37	11	36.7	25	9	HS270340	AJ270340 Homo sapi
38	11	36.7	27	9	HSTCRGV24	X69244 H.sapiens m
39	11	36.7	30	6	AR142066	AR142066 Sequence
40	11	36.7	30	6	I59933	I59933 Sequence 60
41	11	36.7	30	6	I86791	I86791 Sequence 60
42	11	36.7	30	6	I95816	I95816 Sequence 60
43	11	36.7	30	9	HSTCRGV22	X69242 H.sapiens m
44	11	36.7	30	9	S72587	S72587 TCR gamma =
45	11	36.7	30	9	S72591	S72591 TCR gamma =

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES

AR063829
 Sequence 5 from patent US 5846723.
 AR063829
 AR063829.1 GI:5993137
 Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 30)
 Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
 Methods for detecting the RNA component of telomerase
 Patent: US 5846723-A 5 08-DEC-1998;
 Location/Qualifiers

linear PAT 29-SEP-1999

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source
1. .30
/organism="unknown"
BASE COUNT      6 a   10 c   9 g   5 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 30; DB 6; Length 30;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30
        |||||
Db       1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

RESULT 2
AR063830
LOCUS      AR063830      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5846723.
ACCESSION AR063830
VERSION    AR063830.1 GI:5993138
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 6 08-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="unknown"
BASE COUNT      5 a   8 c   3 g   4 t
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
        |||||
Db       1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
AR063831
LOCUS      AR063831      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5846723.
ACCESSION AR063831
VERSION    AR063831.1 GI:5993139
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 7 08-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="unknown"
BASE COUNT      3 a   7 c   6 g   4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCAACTCTTCGGGTGGCAG 30
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Db       1 CCAACTCTTCGGGTGGCAG 30

RESULT 4

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128704
LOCUS      I28704      46 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5573924.
ACCESSION I28704
VERSION    I28704.1 GI:1819480
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   Beckmann,M.Patricia., Goodwin,R.G., Giri,J.G. and Armitage,R.J.
REFERENCE  1 (bases 1 to 46)
AUTHORS    Beckmann,M.Patricia., Goodwin,R.G., Giri,J.G. and Armitage,R.J.
TITLE      CD27 ligand
JOURNAL    Patent: US 5573924-A 7 12-NOV-1996;
FEATURES   Location/Qualifiers
            source
            1. .46
            /organism="unknown"
BASE COUNT      6 a   12 c   14 g   14 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 13; DB 6; Length 46;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AACTCTTCGGGT 25
        |||||
Db       25 AACTCTTCGGGT 37

RESULT 5
AB069038
LOCUS      AB069038      20 bp      DNA      linear      SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-A008044
at lp36.
ACCESSION AB069038
VERSION    AB069038.1 GI:15129842
KEYWORDS   synthetic construct DNA.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
TITLE      A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
JOURNAL    Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
REFERENCE  2 (bases 1 to 20)
AUTHORS    Horii,A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            misc_feature
            1. .20
            /note="forward primer for human STS sts-A008044 at lp36
            sts-A008044 obtained from clones B316C6, B132G19, B375M9,
            Human BAC library RPCI-11"
BASE COUNT      4 a   8 c   1 g   7 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 12; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCCCAACTCTTC 20
        |||||
Db       2 GCCCAACTCTTC 13

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RESULT 6
LOCUS AX109246
DEFINITION Sequence 13 from Patent WO0125269.
ACCESSION AX109246
VERSION AX109246.1 GI:13924119
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and Venema,J.
TITLE Human g-protein coupled receptor
JOURNAL Patent: WO 0125269-A 13 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
FEATURES
source 1..26
/organism="synthetic construct"
/db_xref="taxon:32630"
variation 21
/notes="Degenerated primers"
variation 24
/notes="A,C,G or T"
BASE COUNT 1 a 7 c 9 g 5 t 4 others
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCTTCGCGTGG 27
Db 5 TCTTCGCGTGG 16

RESULT 7
LOCUS S72525/c
DEFINITION TCR V gamma 9-T cell receptor gamma chain [V-J junction] [human,
ACCESSION S72525
VERSION S72525.1 GI:240432
KEYWORDS mRNA Partial Mutant, 28 nt].
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 28)
AUTHORS Holroyd,K.J., Tamura,N., Banks,T., Kirby,M., Okayama,H. and
Crystal,R.G.
TITLE Limited diversity of gamma delta T-cell antigen receptor junctional
region sequences in individuals with sarcoidosis compared to broad
diversity in normal subjects
JOURNAL Trans. Assoc. Am. Physicians 103, 102-111 (1990)
MEDLINE 92087348
PUBMED 2151899
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI Gbbsq 72525] from the original journal article.
This sequence comes from Figure 4.
FEATURES
source 1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..>28
/gene="TCR V-gamma>9"
/notes="T cell receptor gamma chain"
<1..>28
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/notes="This sequence comes from Figure 4; conceptual
translation differs from the translation presented in the

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manuscript"
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/product="T cell receptor gamma chain"
/protein_id="AAB20598.2"
/db_xref="GI:7717239"
/translation="PLWERELG"
BASE COUNT 5 a 4 c 13 g 6 t
ORIGIN
Query Match 40.0%; Score 12; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
Db 28 GCCCAACTCTTC 17

RESULT 8
LOCUS HSTCRGV33/c
DEFINITION H.sapiens mRNA for rearranged TCR-gamma chain V region (VJ).
ACCESSION X69253
VERSION X69253.1 GI:510639
KEYWORDS J-region; N-region; T-cell receptor; T-cell receptor gamma chain;
V-region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 30)
AUTHORS Hvass,J.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1992) J. Hvass, La Trobe University,
Neuroimmunology Lab., Dept. of Psych., La Trobe University,
Bundoora, Victoria 3083, AUSTRALIA
REFERENCE 2 (bases 1 to 30)
AUTHORS Hvass,J., Oksenberg,J.R., Fernando,R., Steinman,L. and Bernard,C.C.
TITLE Gamma delta T cell receptor repertoire in brain lesions of patients
with multiple sclerosis
JOURNAL J. Neuroimmunol. 46 (1-2), 225-234 (1993)
MEDLINE 93367035
PUBMED 8395544
FEATURES
source 1..30
/organism="Homo sapiens"
/isolate="MS patient SEL"
/db_xref="taxon:9606"
/clone="MSSELBRASG"
/tissue_type="brain"
misc_feature 1..11
/notes="V-gamma-2 segment"
misc_feature 12..16
/notes="N region"
misc_feature 17..30
/notes="J-gamma-1.2 segment"
BASE COUNT 8 a 4 c 12 g 6 t
ORIGIN
Query Match 40.0%; Score 12; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
Db 27 GCCCAACTCTTC 16

RESULT 9
LOCUS AX158160/c
DEFINITION Sequence 1488 from Patent WO0140521.
ACCESSION AX158160

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VERSION AX158160.1 GI:14539491
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 43)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
JOURNAL Patent: WO 0140521-A 1488 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 18..19
/notes="Nucleotide deleted between bases 18 and 19"
Accession number CG29694531"
misc_feature 19
/notes="2 of 2 allelic variants (1487 is other entry)"
BASE COUNT 10 a 14 c 6 g 13 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
|||||
Db 28 GACAGAGCCCAA 17

RESULT 10
AX158162/c
LOCUS AX158162 46 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1490 from Patent WO0140521.
ACCESSION AX158162
VERSION AX158162.1 GI:14539493
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 46)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
JOURNAL Patent: WO 0140521-A 1490 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1..46
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 21..22
/notes="Nucleotide deleted between bases 21 and 22"
Accession number CG29694531"
misc_feature 22
/notes="2 of 2 allelic variants (1489 is other entry)"
BASE COUNT 10 a 15 c 6 g 15 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
|||||
Db 28 GACAGAGCCCAA 17

RESULT 11
AX024597
LOCUS AX024597 50 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 13 from Patent WO028021.
ACCESSION AX024597
VERSION AX024597.1 GI:10184737
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 50)
AUTHORS Turecek,P., Scheiflinger,F., Schwarz,H.P., Lenting,P.J., van
Mourik,J.A., Pannekoek,H. and Mertens,K.
TITLE A factor viii-polypeptide with factor viii:c-activity
METHODS Patent: WO 0028021-A 13 18-MAY-2000;
JOURNAL BAXTER AKTIEGESELLSCHAFT (AT) ; TURECEK PETER (AT) ; SCHEIFLINGER
FRIEDRICH (AT) ; SCHWARZ HANS PETER (AT) ; LENTING PETRUS JOHANNES
(NL) ; MOURIK JAN AART VAN (NL) ; PANNEKOEK HANS (NL) ; MERTENS
KOENRAAD (NL)
FEATURES
source
1..50
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="Oligonucleotide"
BASE COUNT 11 a 16 c 15 g 8 t
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Query Match 40.0%; Score 12; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCT 18
|||||
Db 31 GAGCCCAACTCT 42

RESULT 12
AX14857/c
LOCUS AX14857 12 bp DNA linear PAT 16-MAY-1994
DEFINITION Nucleotide sequence 1 from patent number EP0334694.
ACCESSION AX14857
VERSION AX14857.1 GI:512100
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cravador,A., De Vos-Pierreux,M.J. and Bollen,A.
TITLE Nucleic acid probes with non-radioactive labels, and preparation
METHODS processes
JOURNAL Patent: EP 0334694-A 1 27-SEP-1989;
IRE-CELLTARG S.A.; LA REGION WALLONNE
FEATURES
source
1..12
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 4 c 4 g 4 t
ORIGIN
Query Match 36.7%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 11 GACAGAGCCCA 1

RESULT 13
AR056247
LOCUS AR056247 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 451 from patent US 5837542.
ACCESSION AR056247
VERSION AR056247.1 GI:5981824
KEYWORDS

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SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
 JOURNAL Patent: US 5837542-A 451 17-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..15
 BASE COUNT 3 a 6 c 1 g 5 t
 ORIGIN

Query Match 36.7%; Score 11; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20
 Db 1 CCCAACTCTTC 11

RESULT 14
 AR114005
 LOCUS 15 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 451 from patent US 6132967.
 ACCESSION AR114005
 VERSION AR114005.1 GI:14094327
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
 TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
 JOURNAL Patent: US 6132967-A 451 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1..15
 BASE COUNT 3 a 6 c 1 g 5 t
 ORIGIN

Query Match 36.7%; Score 11; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20
 Db 1 CCCAACTCTTC 11

RESULT 15
 A32455
 LOCUS 18 bp DNA linear PAT 07-MAY-1996
 DEFINITION Synthetic papillomavirus type 16 E7 probe.
 ACCESSION A32455
 VERSION A32455.1 GI:1567446
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cros,P., Allibert,P.A., Mandrand,B.F. and Dalbon,P.T.
 TITLE Method for immobilizing a nucleic acid fragment by passive adsorption on a solid support, solid support obtained therefrom and its utilisation
 JOURNAL Patent: EP 0524864-A 10 27-JAN-1993;
 FEATURES Location/Qualifiers
 source 1..18

/organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 5 a 7 c 4 g 2 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 5.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGGCCA 13
 Db 4 GACAGAGGCCA 14

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	19	AAV41172 RNA component of h
2	20	66.7	20	19	AAV41173 RNA component of h
3	20	66.7	20	19	AAV41174 RNA component of h
4	14	46.7	26	20	AAV71131 PCR primer htr S32
5	14	46.7	30	21	AAAG1649 Mouse Elf-1 revers
6	13	43.3	46	19	AAV24750 Human Type II IL-1
7	12	40.0	20	24	ABL43397 Human chromosome 1
8	12	40.0	21	20	AAZ23852 Rye microsatellit
9	12	40.0	21	20	AAZ36927 S. cereale microsa

10	12	40.0	24	20	AAZ36173	PCR primer used to
11	12	40.0	26	22	AAF80328	PCR primer for cDN
12	12	40.0	43	22	AAI74547	Human silent SNP c
13	12	40.0	46	22	AAI74549	Human silent SNP c
14	12	40.0	50	21	AA440237	Construct pC2-m9H5
15	11	36.7	12	23	AB141062	Oligonucleotide pr
16	11	36.7	13	20	AAK00290	Target DNA sequenc
17	11	36.7	13	23	ABF03254	Oligonucleotide SE
18	11	36.7	13	23	ABF03255	Oligonucleotide SE
19	11	36.7	13	23	ABH33140	Oligonucleotide SE
20	11	36.7	13	23	ABH33141	Oligonucleotide SE
21	11	36.7	15	16	AAZ52289	Mouse ICAM hammerh
22	11	36.7	18	13	AAQ20414	Detection probe #2
23	11	36.7	18	14	AAQ36192	Detection probe fo
24	11	36.7	20	10	AAH97152	HPV-16 primer (694
25	11	36.7	20	10	AAH94234	Sequence of probe
26	11	36.7	20	11	AAQ06516	Probe/primer TB-5
27	11	36.7	20	13	AAQ22888	HCV-Hc59 primer #6
28	11	36.7	20	17	AAZ36613	5' primer for huma
29	11	36.7	20	22	AAQ05954	Human diacylglycer
30	11	36.7	20	24	ABL43707	Human chromosome 1
31	11	36.7	21	15	AAQ62049	Hen egg white lyso
32	11	36.7	21	19	AAV52648	Hepatocyte nuclear
33	11	36.7	21	21	AAZ77184	Human biallelic ma
34	11	36.7	21	22	AAH01363	aac(3')-Iib resist
35	11	36.7	21	22	AAF95841	Human gene single
36	11	36.7	21	24	ABA91189	Collectin PCR prim
37	11	36.7	22	21	AAC68689	Mouse R35 specific
38	11	36.7	22	22	AAC01361	aac(3')-Iib resist
39	11	36.7	22	24	ABK86775	PCR primer, 2815,
40	11	36.7	23	21	AAQ09876	Human papillomavir
41	11	36.7	24	10	AAH97159	HPV probe. Synthe
42	11	36.7	24	10	AAH94236	Sequence of probe
43	11	36.7	24	22	AAF64166	Primer #106. Homo
44	11	36.7	24	24	ABQ02087	Oligonucleotide ad
45	11	36.7	24	24	ABQ02284	Oligonucleotide ad

ALIGNMENTS

RESULT 1
AAV41172 standard; DNA; 30 BP.

AC AAV41172;
XX AAV41172;
XX 08-OCT-1998 (first entry)

RNA component of human telomerase (htr) antisense oligo 16.

RNA component; human telomerase; antisense oligonucleotide; infection;
neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
contraction; sterilisation; immunosuppression; therapeutic; htr;
immune system down-regulation; anti-inflammatory therapy; ss.

OS Synthetic.
OS Homo sapiens.

XX WO9828442-A1.

XX 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

XX 20-DEC-1996; 96US-0770564.

PA (GERO-) GERON CORP.

XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

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XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
Db 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
RESULT 2
AAV41173
ID AAV41173 standard; DNA; 20 BP.
XX
XX AAV41173;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 16ab.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
Db 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
RESULT 2
AAV41173
ID AAV41173 standard; DNA; 20 BP.
XX
XX AAV41173;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 16bc.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
SQ
Query Match 66.7%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20
RESULT 3
AAV41174
ID AAV41174 standard; DNA; 20 BP.
XX
XX AAV41174;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 16bc.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
SQ
Query Match 66.7%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

```


PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;
Query Match 66.7%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 CCAACTCTTCGGGTGGCAG 30
DB 1 CCAACTCTTCGGGTGGCAG 20
RESULT 4
ID AAX77131/c
XX AAX77131 standard; DNA; 26 BP.
AC AAX77131;
XX
XX
XX 03-AUG-1999 (first entry)
XX PCR primer hTR S328.
XX
XX Cellular senescence; modulator; G6 gene; senescent gene expression;
KW pG6; human; PCR primer; ss.
XX Synthetic.
OS
XX WO9925878-A2.
PN
XX
XX 27-MAY-1999.
XX
XX 19-NOV-1998; 98WO-US24996.
XX
XX 19-NOV-1997; 97US-0974180.
XX
XX (GERO-) GERON CORP.
PA
XX Funk W;
PI
XX WPI; 1999-347496/29.
DR
XX New human G6 gene, useful for identifying agents for treating
PT diseases and/or conditions associated with cell senescence
PT
XX Example 5; Page 74; 79pp; English.
XX The invention relates to methods for modulating and identifying cellular

senescence. Recombinant expression vectors comprising a recombinant
polynucleotide corresponding to a polynucleotide in a human G6 gene, are
useful for altering senescent gene expression. The vectors and host cells
comprising the vectors are useful for identifying agents that prevent or
modulate senescent gene expression. The polynucleotides are useful for
producing the protein, pG6 and nucleic acid derivatives. The proteins
encoded are useful for raising antibodies specific for pG6, which are
useful for isolating pG6, and for detecting cells comprising pG6 in
complex cell mixtures. The characterization of the polynucleotides enable
the identification of therapeutic agents that identify and distinguish
between young and senescent cells. This enables treatment of aging
diseases induced or exacerbated by cellular senescence.
XX
SQ Sequence 26 BP; 1 A; 8 C; 9 G; 8 T; 0 other;
Query Match 46.7%; Score 14; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAA 14
DB 14 CTGACAGAGCCCAA 1
RESULT 5
ID AAA61649/c
XX AAA61649 standard; DNA; 30 BP.
AC AAA61649;
XX
XX 23-OCT-2000 (first entry)
DT
XX Mouse Elf-1 reverse PCR primer.
DE
XX
XX Elf-1; mouse; transcriptional regulatory factor; rat;
KW polynorphic variant; immunological disease; allergic disease;
KW PCR primer; ss.
XX
XX Mus sp.
OS
XX JP2000135088-A.
PN
XX 16-MAY-2000.
PD
XX 30-OCT-1998; 98JP-0309595.
XX
XX 30-OCT-1998; 98JP-0309595.
PR
XX (ASAK) ASAHI BREWERIES LTD.
PA
XX WPI; 2000-425802/37.
XX
XX A transcription regulating factor Elf-1 cDNA and its polymorphism -
PT
XX Example 1; Page 4; 21pp; Japanese.
XX The invention relates to three polymorphic variants of a rat
CC transcriptional regulatory factor Elf-1 (AAB03190-B03192) and nucleic
CC acids encoding them (AAA61645-A61647). The invention also encompasses
CC the use of Elf-1 for regulating the transcription of a gene in an
CC expression vector. The cDNA encoding rat Elf-1 variant #1 (AAA61645)
CC was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1
CC cDNA, and the rat Elf-1 variant #2 and #3 cDNAs (AAA61646-A61647) were
CC subsequently isolated. The Elf-1 cDNA and protein sequences are
CC potentially useful for the prevention and treatment of immunological and
CC allergic diseases mediated by Elf-1. Sequences AAA61648-A61649 represent
CC mouse Elf-1 PCR primers used in an exemplification of the invention to
CC isolate rat Elf-1 variant #1 cDNA.
XX
SQ Sequence 30 BP; 9 A; 4 C; 7 G; 10 T; 0 other;
Query Match 46.7%; Score 14; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AGAGCCCACTCTT 19
DB 19 AGAGCCCACTCTT 6

RESULT 6
AAV34750
ID AAV34750 standard; DNA; 46 BP.
XX
AC AAV34750;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human Type II IL-1R primer #3.
XX

KW Type II interleukin-1 receptor; IL-1R; immune response; inflammation;
KW regulation; soluble; cell surface receptor; treatment; alloantigen;
KW tissue; organ; rejection; transplant; graft-versus-host disease; human;
KW autoimmune dysfunction; T-cell activation; self antigen; primer;
KW rheumatoid arthritis; diabetes mellitus; multiple sclerosis; ss.
XX

OS Synthetic.

OS Homo sapiens.

PN US5767064-A.

XX 16-JUN-1998.

PD 16-MAY-1995; 95US-0442043.

XX 16-MAY-1991; 91US-0701415.

XX 05-JUN-1990; 90US-0534193.

XX 24-AUG-1990; 90US-0573576.

XX 13-DEC-1990; 90US-0627071.

XX 12-JUL-1993; 93US-0091519.

XX 13-MAY-1994; 94US-0242211.

XX 16-MAY-1995; 95US-0442043.

XX (IMMV) IMMUNEX CORP.

XX Cosman DJ, Dower SK, Lupton SD, Mosley BA, Sims JE;

XX WPI; 1998-361746/31.

XX Regulation of interleukin-1 mediated immune or inflammatory response

XX in mammal - comprises administering soluble IL-1 receptor protein,

XX used in treatment of e.g. graft versus host disease and multiple

XX sclerosis

XX Example 1; Column 19; 33pp; English.

XX AAV34748-V34756 are primers used in the isolation of human and mouse

XX type II interleukin-1 receptor (IL-1R) which is used in a method to

XX investigate the regulation of the immune or inflammatory response in a

XX mammal. This method involves administering a soluble type-II IL-1

XX receptor protein in an amount effective to bind to IL-1 and prevent its

XX binding to cell-surface IL-1 receptors. The process can be used for

XX treating alloantigen-induced rejection of transplanted tissues or

XX organs, graft-versus-host disease and autoimmune dysfunction dependent

XX upon the activation of T cells against self antigens, selected from

XX rheumatoid arthritis, diabetes mellitus or multiple sclerosis.

XX Sequence 46 BP; 6 A; 12 C; 14 G; 14 T; 0 other;

XX Query Match 43.3%; Score 13; DB 19; Length 46;

XX Best Local Similarity 100.0%; Pred. NO. 4.2e+02;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 13 AACTCTTCGGGT 25

XX 25 AACTCTTCGGGT 37

RESULT 7

ABL43397

ID ABL43397 standard; DNA; 20 BP.

XX ABL43397;

XX 11-APR-2002 (first entry)

XX Human chromosome 1p36-35 PCR primer SEQ ID NO:441.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;

XX genome; PCR primer; ss.

XX Homo sapiens.

XX JP2001321190-A.

XX 20-NOV-2001.

XX 12-MAR-2001; 2001JP-0068285.

XX 10-MAR-2000; 2000JP-0066716.

XX (RIKA) RIKAGAKU KENKYUSHO.

XX (GENO-) GENOTEX YG.

XX WPI; 2002-144136/19.

XX Arraying genome clones -

XX Claim 4; Page 13; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The

XX method comprises: (a) clones of the genomic libraries contained in

XX multiwell plates numbered for discrimination are mixed in each of the

XX multiwell plates; (b) a primer designed based on the chromosome marker

XX sequence is added to the mixture to carry out an amplification reaction;

XX (c) a signal corresponding to the marker is detected from the resultant

XX amplified product to specify the discrimination Nos. of the multiwell

XX plates containing the clones having said marker sequence; (d) the order

XX of the markers is changed so that the same discrimination Nos. succeed to

XX the maximum in the specified discrimination Nos. to array the multiwell

XX plates; (e) the clones in the multiwell plates of the specified

XX discrimination Nos. are mixed respectively in each well of longitudinal

XX and lateral directions; (f) the mixed clones are cultured and the

XX resultant cultures are amplified by using the above primer; (g) signals

XX are detected from the amplified products; (h) the clones in the multiwell

XX plates are specified from the detected result; and (i) the clones are

XX reconstituted as the positions on the chromosome and arrayed. The

XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent

XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634

XX represent PCR primers for human chromosome 21q22.1, which are

XX specifically claimed for use in the present invention.

XX Sequence 20 BP; 4 A; 8 C; 1 G; 7 T; 0 other;

XX Query Match 40.0%; Score 12; DB 24; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 9 GCCCAACTCTTC 20

XX 2 GCCCAACTCTTC 13

XX RESULT 8

AAZ23852

ID AAZ23852 standard; DNA; 21 BP.

XX AAZ23852;

XX AAZ23852;

XX

```

DT 21-JAN-2000 (first entry)
XX
DE Rye microsatellite marker 13 PCR primer 2.
XX
XX Microsatellite marker; rye; hypervariable genomic region; Poaceae;
KW Triticeae; breeding program; DNA fingerprinting; variety; detection;
KW self pollination; cross pollination; cytoplasmic line; genetic mapping;
KW polymorphism; PCR primer; ss.
XX
OS Synthetic.
OS Secale cereale.
XX
XX DE19811506-A1.
XX
XX 21-OCT-1999.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX WPI; 1999-591715/51.
XX
XX New microsatellite markers for rye and closely related grasses, used
PT for genetic analysis and in breeding
XX
XX Claim 6; Page 27; 28pp; German.
XX
CC This invention describes novel microsatellite markers (MSM), based on
CC the hypervariable genomic regions of rye (Secale cereale) and of plants
CC from the tribes Triticeae and Poaceae. MSM, which are new genetic markers
CC for rye and closely related species, are used for genetic analysis and
CC in breeding programs. Typical applications are in DNA fingerprinting;
CC identification of varieties; detection of self and cross pollination;
CC characterization of cytoplasmic lines, and genetic mapping (of mono- or
CC poly-genic traits). MSM show a higher degree of polymorphism than known
CC markers (both within and between different rye varieties and lines); can
CC be detected by polymerase chain reaction, so that even very small
CC samples may be analyzed, and generate many alleles per marker locus.
CC AAZ23827-723886 represent the microsatellite marker PCR primers
CC described in the method of the invention.
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
Query Match 40.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0;

QY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 9
AA36927
ID AAX36927 standard; DNA; 21 BP.
XX
AC AAX36927;
XX
XX 02-JUL-1999 (first entry)
XX
XX S. cereale microsatellite marker PCR primer 26.
XX
XX Microsatellite; marker; PCR primer; rye; plant; Triticeae; Poaceae;
KW simple sequence repeat; SSR; sequence tag site; STS; genetic analysis;
KW DNA fingerprinting; variety identification; self fertilization;
KW detection; cross fertilization; cytological line; gene mapping;
KW monogenic trait; polygenic trait; ss.
XX
XX Synthetic.
OS Secale cereale.
XX
XX DE19835109-A1.
XX
XX 15-APR-1999.
XX
XX 04-AUG-1998; 98DE-1035109.
XX
XX 02-OCT-1997; 97DE-1043671.
XX
XX (GVSE-) GVS GES ERWERB & VERWERTUNG LANDWIRTSCHA.
XX
XX Saal B, Wricke G;
XX
XX WPI; 1999-245522/21.
XX
XX Microsatellite markers derived from the genome of rye, useful for
genetic mapping as markers of monogenic or polygenic traits
XX
XX Claim 6; Page 16; 28pp; German.
XX
CC This invention describes Secale cereale microsatellite markers based on
CC hypervariable genomic segments of Secale cereale and plants of the
CC tribes Triticeae and Poaceae. The microsatellite markers comprise a simple
CC sequence repeat (SSR) marker as sequence tag site (STS), defined by two
CC specific S. cereale defined primers, of mean length 18-26 bases and
CC flanking the microsatellite sequence (MSS). Such markers are useful for
CC genetic analysis of rye, triticale and other species of the tribes
CC Triticeae and Poaceae, e.g. for DNA fingerprinting; identification of
CC varieties; detecting self or cross fertilization; studying similarity
CC and relatedness; characterization of cytological lines, or generally any
CC sort of gene mapping. Particularly, they are useful for genetic mapping
CC and marking of mono- or poly-genic traits, selection and evaluation of
CC varietal purity or checking culture stages (particularly in hybrid
CC culture methods), purity of propagative materials, success of
CC self-fertilization and required ratio of components in populations and
CC hybrids. AAX36902-X36965 represent PCR primers used in the method of the
CC invention.
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
Query Match 40.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0;

QY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 10
AA36173
ID AAX36173 standard; DNA; 24 BP.
XX
AC AAX36173;
XX
XX 15-JUL-1999 (first entry)
XX
XX PCR primer used to amplify a fragment of ICAM-6 nucleic acid.
XX
XX Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;
KW intercellular adhesion; inflammatory process; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9920762-A1.
XX
XX 29-APR-1999.
XX
XX 22-OCT-1998; 98WO-US22442.
XX
XX 22-OCT-1997; 97US-0955661.
XX
XX (ICOS-) ICOS CORP.
XX

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PI Loughney K, Staunton DE, Vazeau R;
XX WPI; 1999-288308/24.
XX
XX New isolated intercellular adhesion molecule-6 used for, e.g.
XX diagnosis of inflammatory processes
XX
XX Example 15; Page 53; 102pp; English.
XX
XX The specification describes an intercellular adhesion molecule
XX (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides
XX can be used for drug screening and developing products for therapy
XX involving intercellular adhesion, e.g. in inflammatory processes.
XX The products can also be used for detection, diagnosis and the
XX production of transgenic animals. PCR primers AAX36170-73 were used
XX in the course of the invention.
XX
XX Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
SQ
    Query Match      40.0%; Score 12; DB 20; Length 24;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCACAGAGCCCA 13
Db 1 TCACAGAGCCCA 12

RESULT 11
AAF80328
ID AAF80328 standard; DNA; 26 BP.
XX
XX AAF80328;
XX
XX 29-JUN-2001 (first entry)
XX
XX PCR primer for cDNA encoding the G-protein coupled receptor IGS4.
XX
XX Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;
XX nervous system disorder; psychiatric disorder; Parkinson's disease;
XX episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke;
XX cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
XX motility disorder; myocardial infarction; hypertension; dyslipidemia;
XX gastrointestinal disorder; inflammatory bowel disease; osteoporosis;
XX inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
XX gynecological disorder; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200125269-A2.
XX
XX 12-APR-2001.
XX
XX 25-SEP-2000; 2000WO-EF09584.
XX
XX 24-SEP-1999; 99EP-0203140.
XX
XX 24-SEP-1999; 99NL-1013140.
XX
XX 28-JUL-2000; 2000EP-0202683.
XX
XX 31-JUL-2000; 2000US-0222047.
XX
XX (SOLV ) SOLVAY PHARM BV.
XX
XX Deleersnijder W, Berger C, Loeken C, Nys G, Venema J;
XX WPI; 2001-273568/28.
XX
XX New G-protein coupled receptors and the polynucleotides encoding them,
XX useful for preventing, ameliorating or correcting nervous system
XX disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
XX or cancers
XX
XX Example 1a; Page 39; 102pp; English.
XX

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```

CC PCR primers AAF80328-30 were used to amplify cDNA encoding a
CC human G-protein coupled receptor designated IGS4. IGS4 exists in two
CC polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
CC polynucleotides are useful for preventing, ameliorating or correcting
CC dysfunctions or diseases. These diseases include peripheral nervous
CC system, psychiatric and central nervous system disorders
CC (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's
CC disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases
CC (e.g. heart failure, angina pectoris, myocardial infarction or
CC hypertension), dyslipidemias, obesity, emesis, gastrointestinal
CC disorders (e.g. inflammatory bowel disease or motility disorders),
CC osteoporosis, inflammations, infections (e.g. bacterial, fungal,
CC protozoan or viral), pain, cancers, immune disorders, allergies,
CC sepsis or gynecological disorders. Agonists or antagonists of IGS4 are
CC effective with regard to disorders of the nervous system, including the
CC central and peripheral nervous systems, disorders of the gastrointestinal
CC system, cardiovascular system, skeletal muscle, thyroid, lung or
CC genitourinary system, or immunological disease. The IGS4 polynucleotides
CC are useful as diagnostic reagents for detecting under-expression,
CC overexpression or altered expression of IGS4.
XX
XX Sequence 26 BP; 1 A; 7 C; 9 G; 5 T; 4 other;
SQ
    Query Match      40.0%; Score 12; DB 22; Length 26;
    Best Local Similarity 100.0%; Pred. No. 1.6e+03;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCTTCGCGGTGG 27
Db 5 TCTTCGCGGTGG 16

RESULT 12
AAI74547/c
ID AAI74547 standard; DNA; 43 BP.
XX
XX AAI74547;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:1488.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
XX
XX 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy -
XX
XX Claim 1; Page 509; 2653pp; English.
XX
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AAM53114 to AAM53329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX

```

CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

XX Sequence 43 BP; 10 A; 14 C; 6 G; 13 T; 0 other;
 SQ Query Match 40.0%; Score 12; DB 22; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCAA 14
 |||||
 Db 28 GACAGAGCCCAA 17

RESULT 13
 AAI74549/c
 ID AAI74549 standard; DNA; 46 BP.
 XX
 AC AAI74549;
 XX
 DT 09-NOV-2001 (first entry)
 XX Human silent SNP containing nucleic acid SEQ:1490.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 XX Homo sapiens.

XX WO200140521-A2.
 PN
 PD 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32758.
 PF
 XX 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkete RA, Leach M;
 PI
 XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -
 PT
 XX Claim 1; Page 509; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its

CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

SQ Sequence 46 BP; 10 A; 15 C; 6 G; 15 T; 0 other;
 Query Match 40.0%; Score 12; DB 22; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCAA 14
 |||||
 Db 28 GACAGAGCCCAA 17

RESULT 14
 AAA40237
 ID AAA40237 standard; DNA; 50 BP.
 XX
 AC AAA40237;
 XX

DT 02-NOV-2000 (first entry)
 XX Construct pC2-m8#518 primer P-CC(4).
 DE
 XX Factor VIII; light chain; LRP; gene therapy; antihemophilic; blood;

KW low density lipoprotein receptor-related protein; coagulation disorder;
 KW thrombotic system; fibrinolytic system; primer; ss.
 XX Unidentified.

XX WO200028021-A1.
 PN
 XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-AT00272.
 PF
 XX 10-NOV-1998; 98AT-0001872.
 PR (BAXT) BAXTER AG.

XX Lenting PJ, Van Mourik JA, Mertens K, Pannekoek H, Turecek P;
 PI Schwarz H, Scheifflinger F;
 XX WPI; 2000-376538/32.

XX New modified form of factor VIII, useful for treating hemophilia, has
 PT altered binding to low density lipoprotein-related protein, resulting
 PT in extended in vivo half-life -
 XX Example XI; Page 35; 57pp; German.

XX This invention describes a novel factor VIII polypeptide (I) with factor
 CC VIII:C activity which has a modification in at least one of the A3, C1
 CC and/or C2 domains of the light chain that modifies binding affinity to
 CC low density lipoprotein receptor-related protein (LRP). Independent
 CC claims are also included for the following: (1) DNA (II) that encodes
 CC (I); (2) an expression vector containing (II); (3) transformed cells and
 CC their descendants containing (II); (4) recombinant production of (I) by
 CC culturing cells of (C); and (5) pharmaceutical composition containing a
 CC factor VIII molecule (Ia) with factor VIII:C activity plus an LRP
 CC antagonist (III). The products of the invention have antihemophilic
 CC activity. (I) has reduced affinity for LRP, a receptor involved in
 CC clearance of factor VIII from the blood. (I), optionally formulated with
 CC an antagonist of LRP, is used for treatment of coagulation disorders,
 CC specifically hemophilia A. It may also be used to treat subjects with
 CC disorders of the thrombotic or fibrinolytic systems, e.g. before,
 CC during or after surgery. Nucleic acid that encodes (I) can be used

CC similarly in gene therapy. The light chain modifications reduce clearance
CC of factor VIII protein from the blood, resulting in longer in vivo
CC half-life (particularly at least 90% greater than wild type) and
CC increased stability, in vivo or in vitro. The modifications do not
CC adversely affect procoagulant activity. This sequence represents a primer
CC used in the construction of the plasmid pC2-m9#518 which contains the
CC Factor VIII light chain C2 region which is described in the method of the
CC invention.

XX Sequence 50 BP; 11 A; 16 C; 15 G; 8 T; 0 other;

Query Match 40.0%; Score 12; DB 21; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCCCACTCT 18
Db 31 GAGCCCACTCT 42

RESULT 15

ABI41062

ID ABI41062 standard; DNA; 12 BP.

XX AC ABI41062;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 341035 for detecting SNP TSC0010735.

XX KW SNP; single-nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status

PS Claim 1; SEQ ID 341035; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.

XX CC ABI00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 other;

Query Match 36.7%; Score 11; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 5.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CAACCTCTTCGC 22

Db 2 CAACCTCTTCGC 12

Search completed: June 23, 2003, 05:43:36
Job time : 201.67 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 241.076 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-5

Perfect score: 30
Sequence: 1 CTGACAGACCCCACTTCGCGGTGGCAG 30

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	43.3	46	9	US-10-199-209-5
2	12	40.0	25	9	US-10-098-263B-31566
3	12	40.0	25	9	US-10-098-263B-110352
4	12	40.0	31	9	US-09-288-971-6
5	12	40.0	31	9	US-09-288-971-10
6	11	36.7	18	10	US-09-969-373-3187
7	11	36.7	21	9	US-10-222-334-65
8	11	36.7	24	9	US-09-940-185-2094
9	11	36.7	24	9	US-09-940-185-2291
10	11	36.7	24	10	US-09-898-779-110
11	11	36.7	25	9	US-09-992-665-205
12	11	36.7	25	9	US-10-098-263B-97446
13	11	36.7	25	9	US-10-098-263B-129624
14	11	36.7	26	10	US-09-118-276-16
15	11	36.7	36	8	US-08-961-888-12
16	11	36.7	36	9	US-09-824-017-24
17	11	36.7	36	9	US-09-386-118A-24
18	11	36.7	36	9	US-10-002-050-29
19	11	36.7	36	9	US-10-002-304-29

20	11	36.7	36	12	US-10-003-152-29	Sequence 29, Appl
21	11	36.7	38	9	US-09-824-017-25	Sequence 25, Appl
22	11	36.7	38	9	US-09-986-118A-25	Sequence 25, Appl
23	10	33.3	17	9	US-09-818-875-1383	Sequence 1383, Ap
24	10	33.3	17	9	US-09-818-875-1384	Sequence 1384, Ap
25	10	33.3	17	9	US-09-818-875-1387	Sequence 1387, Ap
26	10	33.3	17	9	US-09-818-875-1388	Sequence 1388, Ap
27	10	33.3	19	9	US-10-093-958-22	Sequence 22, Appl
28	10	33.3	19	9	US-10-291-022-2	Sequence 2, Appl
29	10	33.3	20	9	US-09-971-894-12	Sequence 12, Appl
30	10	33.3	20	9	US-10-090-011-45	Sequence 45, Appl
31	10	33.3	20	9	US-09-915-814-161	Sequence 161, Appl
32	10	33.3	20	10	US-09-909-849-17	Sequence 17, Appl
33	10	33.3	20	10	US-09-263-959-1126	Sequence 1126, Ap
34	10	33.3	21	9	US-09-853-526-420	Sequence 420, App
35	10	33.3	21	9	US-10-082-804-3	Sequence 3, Appl
36	10	33.3	21	9	US-09-909-567B-23	Sequence 23, Appl
37	10	33.3	21	9	US-10-085-906-387	Sequence 387, App
38	10	33.3	21	10	US-09-901-484A-420	Sequence 420, App
39	10	33.3	22	9	US-09-487-318-11	Sequence 11, Appl
40	10	33.3	22	10	US-09-930-251-16	Sequence 16, Appl
41	10	33.3	22	10	US-09-930-251-17	Sequence 17, Appl
42	10	33.3	22	10	US-09-930-251-18	Sequence 18, Appl
43	10	33.3	23	9	US-10-090-887-8	Sequence 8, Appl
44	10	33.3	23	10	US-09-808-382-4	Sequence 4, Appl
45	10	33.3	24	9	US-09-940-185-2918	Sequence 2918, Ap

ALIGNMENTS

RESULT 1
US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US20030060616A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; Cosman, David J.
; Lupton, Stephen D.
; Mosley, Bruce A.
; Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5
Query Match 43.3%; Score 13; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
| | | | | | | | | |
DB 25 AACTCTTCGCGGT 37

RESULT 2
US-10-098-263B-31566
; Sequence 31566, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-31566
Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCITTCGCGGTGG 27
| | | | | | | | | |
DB 5 TCITTCGCGGTGG 16

RESULT 3
US-10-098-263B-110352
; Sequence 110352, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110352
Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCG 21
| | | | | | | | | |
DB 3 CCCAACTCTTCG 14

RESULT 4
US-09-288-971-6/c
; Sequence 6, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-6
Query Match 40.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
| | | | | | | | | |
DB 28 CTGACAGAGCCC 17

RESULT 5
US-09-288-971-10
; Sequence 10, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-10
Query Match 40.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
| | | | | | | | | |
DB 4 CTGACAGAGCCC 15

RESULT 6
US-09-969-373-3187
; Sequence 3187, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:

```


; APPLICANT: Effertz, Roger J.
; APPLICANT: Haughe, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3187
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3187

Query Match 36.7%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 7 GCCCAACTCTT 17

RESULT 7

US-10-222-334-65/c
; Sequence 65, Application US/10222334
; Publication No. US20030073116A1
; GENERAL INFORMATION:
; APPLICANT: Gineburg, David
; APPLICANT: Levy, Gallia
; APPLICANT: Tsai, Han-Mou
; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
; FILE REFERENCE: UM-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/312,834
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-222-334-65

Query Match 36.7%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCC 11
Db 11 CTGACAGAGCC 1

RESULT 8

US-09-940-185-2094/c
; Sequence 2094, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948

; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2094
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2094

Query Match 36.7%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCACTCTTCGC 22
Db 11 CCACTCTTCGC 1

RESULT 9

US-09-940-185-2291
; Sequence 2291, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2291
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2291

Query Match 36.7%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCC 12
Db 7 TGACAGAGCCC 17

RESULT 10

US-09-898-779-110/c
; Sequence 110, Application US/09898779
; Patent No. US20020106657A1
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE REFERENCE: 18810-82302
; CURRENT APPLICATION NUMBER: US/09/898,779
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/347,114
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-779-110

Query Match      36.7%; Score 11; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCC 11
Db      19 CTGACAGAGCC 9

RESULT 11
US-09-992-665-205
; Sequence 205, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kara Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-205

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACAGAGCCCA 13
Db      3 GACAGAGCCCA 13

RESULT 12
US-10-098-263B-97446
; Sequence 97446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-97446

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTCCTCGCGGT 25

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-779-110

Query Match      36.7%; Score 11; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCC 11
Db      19 CTGACAGAGCC 9

RESULT 13
US-10-098-263B-129624
; Sequence 129624, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129624

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCAACTCTTCG 21
Db      9 CCAACTCTTCG 19

RESULT 14
US-09-118-276-16
; Sequence 16, Application US/09118276
; Patent No. US20010011381A1
; GENERAL INFORMATION:
; APPLICANT: BABYCHUK, ELENA;
; APPLICANT: KUSHNIR, SERGEI;
; APPLICANT: DE BLOCK, MARC;
; APPLICANT: INZE, DIRK
; TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED
; CELL DEATH IN EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIXBEY, FRIEDMAN, LEEDOM, & FERGUSON
; STREET: 8180 GREENSBORO DRIVE, SUITE 800
; CITY: MCLEAN,
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2" DISKETTE
; COMPUTER: IBM-COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/118,276
; FILING DATE: 17-JUL-1998
; PRIOR APPLICATION DATA: NONE
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH H.
; REGISTRATION NUMBER: 31,196; 43,077
; REFERENCE/DOCKET NUMBER: 6201-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 790-9110
; TELEFAX: (703) 883-0370
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 BASES
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
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TOPOLOGY: LINEAR
US-09-118-276-16

Query Match 36.7%; Score 11; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20
DB 11 CCCAACTCTTC 21

RESULT 15

US-08-961-888-12
; Sequence 12, Application US/08961888
; Patent No. US20010016351A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Kerstien
; APPLICANT: Sorge, Joseph
; TITLE OF INVENTION: No. US20010016351a1 Vector For Gene Expression
; TITLE OF INVENTION: In Prokaryotic And Eukaryotic Systems
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,888
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-7451
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-961-888-12

Query Match 36.7%; Score 11; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCCTCGCGGT 25
DB 11 CTCCTCGCGGT 21

Search completed: June 23, 2003, 20:01:30
Job time : 242.076 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	US-08-770-565-5
2	20	66.7	20	2	US-08-770-565-6
3	20	66.7	20	2	US-08-770-565-7
4	14	46.7	26	3	US-08-974-180-33
5	14	46.7	45	6	5198342-4
6	13	43.3	46	1	US-08-091-519-5
7	13	43.3	46	1	US-08-106-507-7
8	13	43.3	46	1	US-08-442-043A-5
9	13	43.3	46	5	PCT-US91-03478-5
10	11	36.7	15	2	US-08-292-620A-451
11	11	36.7	15	3	US-09-071-845-451
12	11	36.7	18	1	US-08-273-776-12
13	11	36.7	18	1	US-08-255-892-42
14	11	36.7	20	1	US-08-358-995-2
15	11	36.7	20	2	US-08-473-020A-13
16	11	36.7	20	3	US-08-913-547-3
17	11	36.7	21	4	US-08-927-219-29
18	11	36.7	24	4	US-09-347-114A-110
19	11	36.7	30	1	US-08-495-743-60
20	11	36.7	30	1	US-08-495-739-60
21	11	36.7	30	1	US-08-495-741-60
22	11	36.7	30	4	US-08-062-023-60
23	11	36.7	36	4	US-08-944-368A-24
24	11	36.7	36	4	US-09-820-764-24
25	11	36.7	38	1	US-08-664-449-61
26	11	36.7	38	4	US-08-944-368A-25
27	11	36.7	38	4	US-09-820-764-25

c 28	11	36.7	42	4	US-09-051-363-23	Sequence 23, Appli
c 29	10	33.3	11	1	US-07-778-233B-3	Sequence 3, Appli
c 30	10	33.3	11	1	US-07-963-321-3	Sequence 3, Appli
c 31	10	33.3	11	1	US-08-290-641-3	Sequence 3, Appli
c 32	10	33.3	11	1	US-08-548-540-3	Sequence 3, Appli
c 33	10	33.3	11	5	PCT-US96-09809-3	Sequence 3, Appli
c 34	10	33.3	17	2	US-08-292-620A-1733	Sequence 1733, Ap
c 35	10	33.3	17	3	US-09-071-845-1733	Sequence 1733, Ap
c 36	10	33.3	17	4	US-08-584-040-5345	Sequence 5345, Ap
c 37	10	33.3	18	1	US-08-539-252-1	Sequence 1, Appli
c 38	10	33.3	18	1	US-08-436-074-1	Sequence 1, Appli
c 39	10	33.3	18	4	US-09-050-159-5	Sequence 5, Appli
c 40	10	33.3	18	5	PCT-US96-06352-1	Sequence 1, Appli
c 41	10	33.3	18	5	PCT-US96-06583-1	Sequence 1, Appli
c 42	10	33.3	20	2	US-08-578-551-10	Sequence 10, Appli
c 43	10	33.3	20	2	US-08-473-020A-14	Sequence 14, Appli
c 44	10	33.3	20	2	US-09-289-368-52	Sequence 52, Appli
c 45	10	33.3	20	2	US-09-190-982-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.5e-09;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

Db 1 CTGACAGAGCCCACTTCGCGTGGCAG 30

RESULT 2
US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCACTTC 20
Db 1 CTGACAGAGCCCACTTC 20

RESULT 3
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-7

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCAACTCTTCGCGTGGCAG 30
Db 1 CCAACTCTTCGCGTGGCAG 20

RESULT 4
US-08-974-180-33/c
; Sequence 33, Application US/08974180
; Patent No. 6025194
; GENERAL INFORMATION:
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Methods for Modulating and Identifying
; TITLE OF INVENTION: Cellular Senescence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Geron Corporation
; STREET: 230 Constitution Drive
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,180
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaster, Kevin R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 473-7779
; TELEFAX: (650) 473-8654
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..26
; OTHER INFORMATION: /note= "primer hTR S328"
US-08-974-180-33

Query Match          46.7%; Score 14; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACAGAGCCCA 14
Db 14 CTGACAGAGCCCA 1

RESULT 5
5198342-4
; Patent No. 5198342
; APPLICANT: MALIISZEWSKI; CHARLES R.
; TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/548,059
; FILING DATE: 05-JUL-1990
; SEQ ID NO: 4:
; LENGTH: 45
5198342-4

Query Match          46.7%; Score 14; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 CAACTCTTCGCGGT 25
Db 23 CAACTCTTCGCGGT 36

RESULT 6
US-08-091-519-5
; Sequence 5, Application US/08091519
; Patent No. 5350683
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:

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; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-091-519-5

Query Match          43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 AACTCTTCGCGGT 25
Db 25 AACTCTTCGCGGT 37

RESULT 7
US-08-106-507-7
; Sequence 7, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
; US-08-106-507-7

Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
|||||
DB 25 AACTCTTCGCGGT 37

RESULT 8

US-08-442-043A-5
; Sequence 5, Application US/08442043A
; Patent No. 5767064

; GENERAL INFORMATION:

; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/442,043A

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/534,192

; FILING DATE: 05-JUN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/573,576

; FILING DATE: 24-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/627,071

; FILING DATE: 13-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/701,415

; FILING DATE: 16-MAY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/091,519

; FILING DATE: 12-JULY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/242,211

; FILING DATE: 13-MAY-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2003-F

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-5570

; TELEFAX: 206-233-0644

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 46 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: N

; ANTI-SENSE: N

; US-08-442-043A-5

Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
|||||
DB 25 AACTCTTCGCGGT 37

RESULT 9

PCT-US91-03478-5

; Sequence 5, Application PC/TUS9103478

; GENERAL INFORMATION:

; APPLICANT: Sims, John E.

; APPLICANT: Cosman, David J.

; APPLICANT: Lupton, Stephen D.

; APPLICANT: Mosley, Bruce A.

; APPLICANT: Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/03478

; FILING DATE: 19910517

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/534,193

; FILING DATE: 06-JUN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/573,576

; FILING DATE: 24-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/627,071

; FILING DATE: 13-DEC-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Wight, Christopher L.

; REGISTRATION NUMBER: 31680

; REFERENCE/DOCKET NUMBER: 2003-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-5570

; TELEFAX: 206-233-0644

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 46 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: N

; ANTI-SENSE: N

; PCT-US91-03478-5

Query Match 43.3%; Score 13; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AACTCTTCGCGGT 25
Db 25 AACTCTTCGCGGT 37

RESULT 10

US-08-292-620A-451
; Sequence 451, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 451:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-292-620A-451

Query Match 36.7%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20
Db 10 CCCAACTCTTC 20

Db 1 CCCAACTCTTC 11

RESULT 11

US-09-071-845-451
; Sequence 451, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845

CLASSIFICATION:

PRIOR APPLICATION DATA: US/08/292,620
FILING DATE: August 17, 1994

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 451:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-071-845-451

Query Match 36.7%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20

Db 1 CCCAACTCTTC 11

RESULT 12

US-08-273-776-12
; Sequence 12, Application US/08273776
; Patent No. 5510084

GENERAL INFORMATION:
APPLICANT: Cros, Philippe
APPLICANT: Allibert, Patrice Andre
APPLICANT: Dalbon, Pascal Thierry
TITLE OF INVENTION: Process for Immobilizing a Nucleic Acid
TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff and Berridge
STREET: 700 S. Washington St.
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,776
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,953
FILING DATE: 17-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB28083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-273-776-12

Query Match 36.7%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
DB 4 GACAGAGCCCA 14

RESULT 13
US-08-255-892-42
Sequence 42, Application US/08255892
Patent No. 5695926
GENERAL INFORMATION:
APPLICANT: CROS, PHILIPPE
APPLICANT: ALLIBERT, PATRICE
APPLICANT: MALET, FRANCOIS
APPLICANT: MABILAT, CLAUDE
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
TITLE OF INVENTION: TECHNIQUE
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON

GENERAL INFORMATION:
APPLICANT: Cros, Philippe
APPLICANT: Allibert, Patrice Andre
APPLICANT: Dalbon, Pascal Thierry
TITLE OF INVENTION: Process for Immobilizing a Nucleic Acid
TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff and Berridge
STREET: 700 S. Washington St.
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,776
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,953
FILING DATE: 17-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB28083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-273-776-12

Query Match 36.7%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
DB 4 GACAGAGCCCA 14

RESULT 13
US-08-255-892-42
Sequence 42, Application US/08255892
Patent No. 5695926
GENERAL INFORMATION:
APPLICANT: CROS, PHILIPPE
APPLICANT: ALLIBERT, PATRICE
APPLICANT: MALET, FRANCOIS
APPLICANT: MABILAT, CLAUDE
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
TITLE OF INVENTION: TECHNIQUE
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON

GENERAL INFORMATION:
APPLICANT: Akio YAMANE
TITLE OF INVENTION: Microtiter Well For Detecting
TITLE OF INVENTION: Nucleic Acid
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,995
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,572
FILING DATE: January 14, 1993
APPLICATION NUMBER: 07/722,673
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.

GENERAL INFORMATION:
APPLICANT: Akio YAMANE
TITLE OF INVENTION: Microtiter Well For Detecting
TITLE OF INVENTION: Nucleic Acid
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,995
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,572
FILING DATE: January 14, 1993
APPLICATION NUMBER: 07/722,673
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.

GENERAL INFORMATION:
APPLICANT: Akio YAMANE
TITLE OF INVENTION: Microtiter Well For Detecting
TITLE OF INVENTION: Nucleic Acid
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,995
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,572
FILING DATE: January 14, 1993
APPLICATION NUMBER: 07/722,673
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.

STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,892
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/834,543
FILING DATE: 11-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: DEEVER, DONALD B.
REGISTRATION NUMBER: 23,048
REFERENCE/DOCKET NUMBER: 1032/94109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-255-892-42

Query Match 36.7%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
DB 4 GACAGAGCCCA 14

RESULT 14
US-08-358-995-2/c
Sequence 2, Application US/08358995
Patent No. 5741638
GENERAL INFORMATION:
APPLICANT: Akio YAMANE
TITLE OF INVENTION: Microtiter Well For Detecting
TITLE OF INVENTION: Nucleic Acid
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,995
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,572
FILING DATE: January 14, 1993
APPLICATION NUMBER: 07/722,673
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "having biotin at
OTHER INFORMATION: 5' end with a spacer"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-358-995-2

Query Match 36.7%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
Db 18 GACAGAGCCCA 8

RESULT 15

US-08-473-020A-13/c
Sequence 13, Application US/08473020A
Patent No. 5877273
GENERAL INFORMATION:

APPLICANT: Hance, Allan J
APPLICANT: Grandchamp-Desraux, Bernard
APPLICANT: Levy-Frebault, Veronique
APPLICANT: Gicquel, Brigitte
TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
TITLE OF INVENTION: applications to the synthesis or detection of nucleic

TITLE OF INVENTION: acids, products of expression of such sequences and
TITLE OF INVENTION: application as immunogenic compositions.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,020A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-473-020A-13

Query Match 36.7%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 CGCGGTGGCAG 30
Db 11 CGCGGTGGCAG 1

Search completed: June 23, 2003, 10:17:05
Job time : 48.9721 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGACCCCACTTCGCGGTGGCAG 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
 PCT-US97-23619-5
 ; Sequence 5, Application PC/TUS9723619
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
 ; TITLE OF INVENTION: RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/23619
 ; FILING DATE: Not yet assigned
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,564
 ; FILING DATE: 20-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,565
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 15389-27PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..30
 ; OTHER INFORMATION: /note="oligo 16"
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 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
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 DB 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30
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 US-08-770-564A-5
 ; Sequence 5, Application US/08770564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ron
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
 ; TITLE OF INVENTION: Against the RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,564A
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; MOLECULE TYPE: DNA
 US-08-770-564A-5
 Query Match 100.0%; Score 30; DB 11; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30
 DB 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30
 RESULT 3
 US-08-521-634-15/c

Sequence 15, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

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Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24 GACAGAGCCCAACTCTTCGGGGT 1

RESULT 4
PCT-US97-23619-6
Sequence 6, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 16ab"
PCT-US97-23619-6
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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTGACAGAGCCCAACTCTTC 20
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PCT-US97-23619-7
Sequence 7, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 16bc"
PCT-US97-23619-7

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCAACTCTTCGCGTGGCAG 20

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US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 7
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US


```
US-09-956-604-105231/c
; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-105231

Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CAACTCTTCGCGGTGGCA 29
DB 21 CAACTCTTCGCGGTGGCA 4

RESULT 9
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CAACTCTTCGCGGTGGCA 29
DB 21 CAACTCTTCGCGGTGGCA 4

US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231
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Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CAACTCTTCGCGGTGGCA 29
DB 21 CAACTCTTCGCGGTGGCA 4

RESULT 11
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          60.0%; Score 18; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CAACTCTTCGCGGTGGCA 29
DB 21 CAACTCTTCGCGGTGGCA 4

RESULT 12
US-09-396-196F-124326
; Sequence 124326, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-124326

Query Match          43.3%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAA 14
DB 2 TGACAGAGCCCAA 14

RESULT 13
US-09-396-196G-124326
```

```
; Sequence 124326, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124326

Query Match      43.3%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAAA 14
      |||||
Db      2 TGACAGAGCCCAAA 14

RESULT 14
US-09-660-220-66821/c
; Sequence 66821, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 66821
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66821

Query Match      43.3%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTC 17
      |||||
Db      16 CAGAGCCCAACTC 4

RESULT 15
US-09-660-220-66822/c
; Sequence 66822, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 66822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66822

Query Match      43.3%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTC 17
      |||||
Db      13 CAGAGCCCAACTC 1

Search completed: June 23, 2003, 16:08:18
Job time : 2517.25 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 1316.89 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-5

Perfect score: 30

Sequence: 1 CTGACAGAGCCCAACTTCGCGGTGGCAG 30

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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11: /cgn2_6/prodata/1/pna/US60_NEW COMB.seq.*
12: /cgn2_6/prodata/1/pna/US60_NEW COMB.seq2.*
13: /cgn2_6/prodata/1/pna/US60_NEW COMB.seq3.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	73.3	23	1	PCT-US03-04088-522
C 2	19	63.3	21	1	PCT-US03-04088-540
C 3	19	63.3	21	1	PCT-US03-04088-544
C 4	19	63.3	21	1	PCT-US03-04088-548
C 5	19	63.3	21	1	PCT-US03-04088-552
C 6	19	63.3	21	1	PCT-US03-04088-556
C 7	19	63.3	21	1	PCT-US03-04088-560
C 8	18	60.0	19	1	PCT-US03-04088-23
C 9	18	60.0	21	1	PCT-US03-04088-287
C 10	16	53.3	21	1	PCT-US03-04088-588
C 11	16	53.3	23	1	PCT-US03-04088-530
C 12	14	46.7	21	1	PCT-US03-04088-258
C 13	14	46.7	21	1	PCT-US03-04088-593
C 14	14	46.7	25	12	US-60-427-808-47221
C 15	14	46.7	25	12	US-60-427-808-699316
C 16	14	46.7	25	12	US-60-427-836-401411
C 17	14	46.7	25	12	US-60-427-836-529892
C 18	13	43.3	19	1	PCT-US03-04088-22
C 19	13	43.3	19	1	PCT-US03-04088-286
C 20	13	43.3	20	1	PCT-US02-21361-189

21	13	43.3	20	9	US-10-188-186-189	Sequence 189, App
22	13	43.3	20	9	US-10-160-619-306	Sequence 306, App
23	13	43.3	20	9	US-10-160-619-315	Sequence 315, App
C 24	13	43.3	25	6	US-09-660-222-66821	Sequence 66821, A
C 25	13	43.3	25	6	US-09-660-222-66822	Sequence 66822, A
C 26	13	43.3	25	6	US-09-660-222-66827	Sequence 66827, A
C 27	13	43.3	25	6	US-09-660-222-66828	Sequence 66828, A
C 28	13	43.3	25	6	US-09-660-222-66829	Sequence 66829, A
C 29	13	43.3	25	9	US-10-355-577-281714	Sequence 281714, A
C 30	13	43.3	25	9	US-10-355-577-534052	Sequence 534052, A
C 31	13	43.3	25	9	US-10-355-577-625356	Sequence 625356, A
C 32	13	43.3	25	12	US-60-427-808-2606	Sequence 2606, App
C 33	13	43.3	25	12	US-60-427-808-435724	Sequence 435724, A
C 34	13	43.3	25	12	US-60-427-808-467623	Sequence 467623, A
C 35	13	43.3	25	12	US-60-427-808-503841	Sequence 503841, A
C 36	13	43.3	25	12	US-60-427-836-95550	Sequence 95550, A
C 37	13	43.3	25	12	US-60-427-836-95550	Sequence 95550, A
C 38	13	43.3	25	12	US-60-427-836-198381	Sequence 198381, A
C 39	13	43.3	25	12	US-60-427-836-331174	Sequence 331174, A
C 40	13	43.3	46	10	US-10-199-209A-5	Sequence 5, Appl1
C 41	12	40.0	21	10	US-10-367-892-14041	Sequence 14041, A
C 42	12	40.0	24	9	US-10-293-338-4756	Sequence 4756, App
C 43	12	40.0	25	6	US-09-660-222-209	Sequence 209, App
C 44	12	40.0	25	6	US-09-660-222-6083	Sequence 6083, App
C 45	12	40.0	25	6	US-09-660-222-27816	Sequence 27816, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTCG 22
 Db 22 CTGACAGAGCCCAACTCTTCG 1

RESULT 2
 PCT-US03-04088-540/c
 ; Sequence 540, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-540
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 540
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-540

Query Match 63.3%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 3
 PCT-US03-04088-544
 ; Sequence 544, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-544
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 544
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-544

Query Match 63.3%; Score 19; DB 1; Length 21;
 Best Local Similarity 78.9%; Pred. No. 0.46;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
 PCT-US03-04088-548/c
 ; Sequence 548, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-548
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 548
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1)

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OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match 63.3% Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 5
PCT-US03-04088-552
Sequence 552, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 552
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match 63.3% Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.46;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 1 UGACAGAGCCCAACUCUUC 19
```

```
RESULT 6
PCT-US03-04088-556/c
Sequence 556, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 556
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
FEATURE:
OTHER INFORMATION: region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(6)
OTHER INFORMATION: 2'-deoxy
FEATURE:
```

```
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3 attached terminal deoxybasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
PCT-US03-04088-556
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 7
PCT-US03-04088-560
Sequence 560, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
FILE REFERENCES: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
```

```
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.46;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19
```

```
RESULT 8
PCT-US03-04088-23/c
Sequence 23, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
FILE REFERENCES: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
```

;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 23
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
;; OTHER INFORMATION: region
PCT-US03-04088-23

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 18 CTGACAGAGCCCACTCT 1

RESULT 9
PCT-US03-04088-287
;; Sequence 287, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 287
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
;; OTHER INFORMATION: region
PCT-US03-04088-287

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.8;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 2 CUGACAGAGCCCAACUCU 19

RESULT 10
PCT-US03-04088-588/c
;; Sequence 588, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 588
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-588

Query Match 53.3%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCTCGCGGTGGCAG 30
| | | | | | | | | | | | | | | | | | | | | |
Db 21 CTCTCGCGGTGGCAG 6

RESULT 11
PCT-US03-04088-530/c
;; Sequence 530, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION-NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 530
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-530

 Query Match 53.3%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 15 CTCTTCGCGGTGGCAG 30
 |||||
 Db 23 CTCTTCGCGGTGGCAG 8

 RESULT 12
 PCT-US03-04088-258/c
 ; Sequence 258, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 258
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-258

Query Match 46.7%; Score 14; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTTCGCGGTGGCAG 30
 |||||
 Db 19 CTTCGCGGTGGCAG 6

 RESULT 13
 PCT-US03-04088-593
 ; Sequence 593, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 593
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
 ; OTHER INFORMATION: antisense region
 PCT-US03-04088-593

 Query Match 46.7%; Score 14; DB 1; Length 21;
 Best Local Similarity 78.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTTCGCGGTGGCAG 30
 |||||
 Db 1 CUUCGCGGUGGCAG 14

 RESULT 14
 US-60-427-808-47221
 ; Sequence 47221, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528-
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 47221
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 US-60-427-808-47221

 Query Match 46.7%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTT 19
 |||||
 Db 2 AGAGCCCAACTCTT 15

RESULT 15

US-60-427-808-699316
 ; Sequence 699316, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 699316
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-699316

Query Match 46.7%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCTTC 20
 |||||
 Db 3 GAGCCCAACTCTTC 16

Search completed: June 23, 2003, 19:12:11
 Job time : 1317.89 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGACCCCACTTCGCGGTGGCAG 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	46	17	AZ379320
C 2	11	36.7	12	13	BM398341
C 3	11	36.7	19	13	BM401213
C 4	11	36.7	20	13	BM395007
C 5	11	36.7	21	17	AZ781467
C 6	11	36.7	22	17	AZ393281

7	11	36.7	24	17	AZ309564
8	11	36.7	26	13	BM399150
9	11	36.7	33	13	BM398611
C 10	11	36.7	34	17	AL759526
C 11	11	36.7	37	13	BJ063841
C 12	11	36.7	40	17	BM398341
C 13	11	36.7	44	13	BM400948
C 14	11	36.7	45	13	BM397151
C 15	11	36.7	47	10	BE536289
C 16	11	36.7	49	9	AA813480
C 17	11	36.7	50	9	AU106839
C 18	10	33.3	14	13	BM396493
C 19	10	33.3	17	13	BM396941
C 20	10	33.3	18	14	BM675715
C 21	10	33.3	20	13	BM400293
C 22	10	33.3	20	13	BM400757
C 23	10	33.3	21	13	BM401335
C 24	10	33.3	22	9	AI687266
C 25	10	33.3	23	17	AZ331549
C 26	10	33.3	23	17	AZ627985
C 27	10	33.3	24	13	BM399103
C 28	10	33.3	25	9	AI647975
C 29	10	33.3	25	13	BM397307
C 30	10	33.3	26	13	BM397299
C 31	10	33.3	28	17	AZ393438
C 32	10	33.3	29	13	BM400082
C 33	10	33.3	29	17	AZ412468
C 34	10	33.3	30	17	AZ310102
C 35	10	33.3	33	13	BM396856
C 36	10	33.3	37	9	AI572041
C 37	10	33.3	37	12	BG423450
C 38	10	33.3	37	13	BI765481
C 39	10	33.3	38	14	H45829
C 40	10	33.3	39	17	AZ773780
C 41	10	33.3	41	13	BM398089
C 42	10	33.3	42	13	BM400119
C 43	10	33.3	42	17	AZ616105
C 44	10	33.3	43	9	AI091574
C 45	10	33.3	44	17	AZ309736

ALIGNMENTS

RESULT 1
AZ379320/c
LOCUS AZ379320 46 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0134P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0134P22 F, DNA sequence.
ACCESSION AZ379320
VERSION AZ379320.1 GI:10493020
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0134 row: P column: 22
 Seq primer: CCTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 46.

FEATURES

source

1. .46
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0134P22"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 15 g 19 t
 ORIGIN
 Query Match 40.0%; Score 12; DB 17; Length 46;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ACAGAGCCCAAC 15
 Db 19 ACAGAGCCCAAC 8

RESULT 2
 BM398341
 LOCUS
 DEFINITION 5009-0-44-D05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398341
 VERSION BM398341.1 GI:18198394
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1. 12
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"

/db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 1 a 4 c 6 g 1 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CGCGGTGGCAG 30
 Db 2 CGCGGTGGCAG 12

RESULT 3
 BM401213
 LOCUS
 DEFINITION 5009-0-84-C02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM401213
 VERSION BM401213.1 GI:18201266
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1. .19
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 5 c 8 g 3 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CGCGGTGGCAG 30
 Db 9 CGCGGTGGCAG 19

RESULT 4
 BM395007
 LOCUS
 DEFINITION 50072-2-7-A08.f.2 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM395007
 VERSION BM395007.1 GI:18195060
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
AUTHORS 1 (bases 1 to 20)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orian, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..20
Location/Qualifiers
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 3 a 7 c 6 g 4 t
ORIGIN

Query Match 36.7%; Score 11; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGGTGGCAG 30
|||||
DB 5 CGCGGTGGCAG 15

RESULT 5
AZ781467/c
LOCUS 21 bp DNA linear GSS 16-FEB-2001
DEFINITION clone UUGC2M0019F23 R, DNA sequence.
ACCESSION AZ781467
VERSION AZ781467.1 GI:12914189
KEYWORDS GSS.
SOURCE house musculus
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: F column: 23
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1..21
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UUGC2M0019F23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 2 a 12 c 12 g 5 t
ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAA 14
|||||
DB 11 ACAGAGCCCAA 1

RESULT 6
AZ393281/c
LOCUS 22 bp DNA linear GSS 03-OCT-2000
DEFINITION clone UUGC1M0156H13 F, DNA sequence.
ACCESSION AZ393281
VERSION AZ393281.1 GI:10508353
KEYWORDS GSS.
SOURCE house musculus
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: H column: 13
Seq primer: CGTTGTAACGACGCCGACGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0156H13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 7 g 7 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAA 14
 |||||
 Db 21 ACAGAGCCCAA 11

RESULT 7
 AZ309564
 LOCUS 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0016E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016E09 F, DNA sequence.
 ACCESSION AZ309564
 VERSION AZ309564.1 GI:10350859
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weisse,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: E column: 09
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0016E09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 4 c 10 g 4 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
 |||||
 Db 8 GACAGAGCCCA 18

RESULT 8
 BM399150
 LOCUS 26 bp mRNA linear EST 17-JAN-2002
 DEFINITION 5009-0-54-All.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM399150
 VERSION BM399150.1 GI:18199203
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..26
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 8 a 5 c 10 g 3 t
 ORIGIN

```

Query Match          36.7%; Score 11; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGGTGGCAG 30
    |||||
Db 16 CGCGGTGGCAG 26

RESULT 9
LOCUS BM398611
DEFINITION 33 bp mRNA linear EST 17-JAN-2002
5009-0-47-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398611
VERSION BM398611.1 GI:18198664
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS Hymenostomatida; Tetrahymena; Tetrahymena.
1 (bases 1 to 33)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobuchner, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL Molecular Genetics and Cell Biology
COMMENT University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4372
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
Location/Qualifiers
1..33
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 5 a 10 c 12 g 6 t
ORIGIN

Query Match          36.7%; Score 11; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGGTGGCAG 30
    |||||
Db 9 CGCGGTGGCAG 19

RESULT 10
LOCUS AL759526/c
DEFINITION 34 bp DNA linear GSS 18-JUN-2002
Arabidopsis thaliana T-DNA flanking sequence GK-188A07-014624,
genomic survey sequence.
ACCESSION AL759526
VERSION AL759526.1 GI:21497874
KEYWORDS GSS.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 34)
Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Atlg07990. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1..34
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-188A07-014624"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 10 a 9 c 9 g 6 t
ORIGIN

Query Match          36.7%; Score 11; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCTTCGCGGTG 26
    |||||
Db 13 TCTTCGCGGTG 3

RESULT 11
LOCUS BJ063841
DEFINITION 37 bp mRNA linear EST 10-DEC-2001
laevis cDNA clone XL077114 5', mRNA sequence.
ACCESSION BJ063841
VERSION BJ063841.1 GI:17471031
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
1 Xenopodinae; Xenopus.
1 (bases 1 to 37)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
JOURNAL Contact: Tadao Shin-i
COMMENT Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

```

```

source
1. 37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="XLO77114"
/library
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 5 a 15 c 3 g 13 t 1 others
ORIGIN
Query Match 36.7%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCG 21
|||||
DB 24 CCAACTCTTCG 34

RESULT 12
LOCUS BH851915.1 40 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_073707.54.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_073707.54.25.x, DNA
sequence.
ACCESSION BH851915
VERSION BH851915.1 GI:21422786
KEYWORDS SOURCE
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 40)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g46110.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1..40
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 7 a 11 c 12 g 10 t
ORIGIN
Query Match 36.7%; Score 11; DB 17; Length 40;

1. 37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 5 a 15 c 3 g 13 t 1 others
ORIGIN
Query Match 36.7%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCG 21
|||||
DB 24 CCAACTCTTCG 34

RESULT 13
LOCUS BM400948 44 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-80-E05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400948
VERSION BM400948.1 GI:18201001
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 44)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology

Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCGGCGGTGGC 28
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DB 27 TTCGGCGGTGGC 17

RESULT 14
LOCUS BM397151 45 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-29-F01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397151
VERSION BM397151.1 GI:18197204
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 45)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology

```


University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES

source

Location/Qualifiers

1. .45
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

10 a 11 c 15 g 9 t

ORIGIN

Query Match 36.7%; Score 11; DB 13; Length 45;

Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGGTGGCAG 30

Db 16 CGCGGTGGCAG 26

RESULT 15

BE536289/c

LOCUS

47 bp mRNA linear EST 09-AUG-2000

DEFINITION

601062681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3448989 5',

mRNA sequence.

ACCESSION

BE536289

VERSION

BE536289.1 GI:9764934

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 47)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM8425 row: a column: 22

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3448989"

/clone_lib="NIH_MGC_10"

/cell_line="MGC36"

/lab_host="DH10B"

/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5 kb. Library prepared by Life

Technologies."

6 a 21 c 10 g 10 t

BASE COUNT

ORIGIN

Query Match

36.7%; Score 11; DB 10; Length 47;

Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13

|||||

Db 34 GACAGAGCCCA 24

Search completed: June 23, 2003, 10:10:19
Job time : 1548.89 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTTTCGGGTGGCAG 30

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338391 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/PCUS COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	30	2	US-08-770-565-5
2	20	66.7	20	2	US-08-770-565-6
3	20	66.7	20	2	US-08-770-565-7
4	15.8	52.7	45	6	5198342-4
5	15.2	50.7	43	1	US-07-797-556-15
6	14.6	48.7	40	2	US-08-425-684-94
7	14.6	48.7	40	2	US-08-675-502-94
8	14.4	48.0	26	2	US-08-859-998-77
9	14.4	48.0	26	4	US-09-225-928-77
10	14.4	48.0	42	4	US-09-051-363-23
11	14.2	47.3	30	1	US-08-285-440-16
12	14.2	47.3	30	1	US-08-630-349-16
13	14.2	47.3	50	2	US-08-920-165-2
14	14	46.7	26	3	US-08-974-180-33
15	13.8	46.0	46	1	US-08-091-519-5
16	13.8	46.0	46	1	US-08-106-507-7
17	13.8	46.0	46	1	US-08-442-043A-5
18	13.8	46.0	46	5	PCT-US91-03478-5
19	13.8	46.0	47	4	US-09-338-907-222
20	13.8	46.0	47	4	US-09-338-907-299
21	13.8	46.0	47	4	US-09-218-207-222
22	13.8	46.0	47	4	US-09-218-207-299
23	13.6	45.3	48	2	US-08-629-039-9
24	13.6	45.3	48	2	US-08-629-039-10
25	13.6	45.3	49	4	US-09-166-966B-3
26	13.4	44.7	32	2	US-08-602-264A-11
27	13.4	44.7	32	3	US-08-461-018A-11

c 28	13.4	44.7	32	4	US-09-216-958-11	Sequence 11, Appl
c 29	13.4	44.7	36	3	US-08-746-883-8	Sequence 8, Appl
c 30	13.2	44.0	30	1	US-08-484-557C-46	Sequence 46, Appl
c 31	13.2	44.0	30	1	US-08-487-426B-46	Sequence 46, Appl
c 32	13.2	44.0	30	2	US-08-487-720A-46	Sequence 46, Appl
c 33	13.2	44.0	36	3	US-08-833-167-69	Sequence 69, Appl
c 34	13.2	44.0	36	4	US-09-344-837A-69	Sequence 69, Appl
c 35	13.2	44.0	45	1	US-08-619-109-1	Sequence 1, Appl
c 36	13.2	44.0	45	2	US-08-878-166-1	Sequence 1, Appl
c 37	13.2	44.0	45	4	US-09-369-635-1	Sequence 1, Appl
c 38	13	43.3	27	1	US-08-196-538-8	Sequence 8, Appl
c 39	13	43.3	30	4	US-09-630-377-3	Sequence 3, Appl
c 40	13	43.3	37	1	US-08-217-327-15	Sequence 15, Appl
c 41	13	43.3	38	1	US-08-472-254A-23	Sequence 23, Appl
c 42	13	43.3	38	2	US-08-477-576B-23	Sequence 23, Appl
c 43	13	43.3	38	2	US-08-428-734B-23	Sequence 23, Appl
c 44	13	43.3	38	4	US-08-713-556F-23	Sequence 23, Appl
c 45	13	43.3	41	1	US-08-058-907-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.3e-05; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 1 CTGACAGAGCCCAACTTTCGGGTGGCAG 30

Db

1

CTGACAGAGCCCAACTCTTCGGCGTGCAG 30

RESULT 2

US-08-770-565-6

Sequence 6, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-6

Query Match 66.7%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

11

CCAACTCTTCGGGTGGCAG 30

Db

1

CCAACTCTTCGGGTGGCAG 20

RESULT 4

5198342-4

Patent No. 5198342

APPLICANT: MALIISZEWSKI, CHARLES R.

TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/548,059

FILING DATE: 05-JUL-1990

SEQ ID NO: 4:

LENGTH: 45

5198342-4

Query Match 52.7%; Score 15.8; DB 6; Length 45;

Best Local Similarity 89.5%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

7

GAGCCCAACTCTTCGCGGT 25

Db

18

GAGGACAACTCTTCGCGGT 36

RESULT 5

US-07-797-556-15/c

Sequence 15, Application US/07797556

Patent No. 5262522

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

;
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-797-556-15

Query Match 50.7%; Score 15.2; DB 1; Length 43;
Best Local Similarity 71.4%; Pred. No. 3e+02; 8; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTCGCGTGGCA 29
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Db 31 TGACAAAGGAAATCTTAGCGCGCGCA 4
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RESULT 6
US-08-425-684-94/c
; Sequence 94, Application US/08425684
; Patent No. 5834252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P. C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN ESQ., TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528J-015400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid

;
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-425-684-94

Query Match 48.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.0%; Pred. No. 5.5e+02; 9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTCGCGTGGCAG 30
|||||
Db 36 TGAGAAAGCGCCACGCTTCCCGAAGGAG 8
|||||

RESULT 7
US-08-675-502-94/c
; Sequence 94, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P. C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,502
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-675-502-94

Query Match 48.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.0%; Pred. No. 5.5e+02; 9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTCGCGTGGCAG 30
|||||
Db 36 TGAGAAAGCGCCACGCTTCCCGAAGGAG 8
|||||

RESULT 8
US-08-859-998-77/c
; Sequence 77, Application US/08859998

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875.
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-225-928-77

Query Match 48.0%; Score 14.4; DB 4; Length 26;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels

QY 7 GAGCCCAACTCTTCGGGTGGCAG 30
DB 24 GAGCGCCTCTCATCGCGGTAGCTG 1

RESULT 10
US-09-051-363-23/c
Sequence 23, Application US/09051363
Patent No. 6270993
GENERAL INFORMATION:
APPLICANT: Shibuya, Masabumi
APPLICANT: Okamoto, Masaji
APPLICANT: Niwa, Mikio
APPLICANT: Matsumoto, Tomoe
APPLICANT: Asano, Makoto
APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,363
FILING DATE: 07-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02906
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 8/211892 JP
FILING DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP

```

;; FILING DATE: 07-OCT-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Ph.D., J.D., Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 06501/012001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: synthetic DNA
US-09-051-363-23

Query Match 48.0%; Score 14.4; DB 4; Length 42;
Best Local Similarity 93.8%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAACTCTT 19
Db 24 ACAGAGCCCAACTCTT 9

RESULT 11
US-08-285-440-16
; Sequence 16, Application US/08285440
; Patent No. 5532337
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,440
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/859,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL:
; ANTI-SENSE: Yes
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-16

Query Match 47.3%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAACTCTTCGGGGTGGCAG 30
Db 2 ACCGAGCTCAAACTTAGTGGGGGAG 28

RESULT 12
US-08-630-349-16
; Sequence 16, Application US/08630349
; Patent No. 5739008
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,349
; FILING DATE: April 10, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,440
; FILING DATE: August 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/858,947

Db
22 ACCGAGCCCTATGCTTCGCGAGTCCAG 48


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; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; US-08-091-519-5

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Query Match      46.0%; Score 13.8; DB 1; Length 46;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 GCCCAACTCTTCGCGGT 25
        | | | | | | | | | |
Db      21 GACAACTCTTCGCGGT 37

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Search completed: June 25, 2003, 00:24:36
Job time : 46.5378 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	49.3	28	9	US-10-151-320-25
2	14.6	48.7	40	10	US-09-245-802-94
3	14.4	48.0	19	9	US-10-093-958-22
4	14.4	48.0	31	10	US-09-801-274-373
5	13.8	46.0	27	9	US-09-733-634-11
6	13.8	46.0	46	9	US-10-199-209-5
7	13.8	46.0	47	9	US-09-853-526-222
8	13.8	46.0	47	9	US-09-853-526-222
9	13.8	46.0	47	10	US-09-901-484A-222
10	13.8	46.0	47	10	US-09-901-484A-222
11	13.6	45.3	24	10	US-09-820-339A-23
12	13.6	45.3	28	9	US-10-152-363A-48
13	13.6	45.3	29	9	US-10-152-363A-41
14	13.6	45.3	29	9	US-10-152-363A-42
15	13.6	45.3	48	9	US-10-152-363A-16
16	13.4	44.7	21	9	US-09-909-567B-23
17	13.4	44.7	23	10	US-09-766-154-31
18	13.4	44.7	25	9	US-10-098-263B-5571
19	13.4	44.7	25	9	US-10-098-263B-47598

ALIGNMENTS

RESULT 1

US-10-151-320-25
; Sequence 25, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436
; CURRENT APPLICATION NUMBER: US/10151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer used for PCR.
US-10-151-320-25

Query Match 49.3%; Score 14.8; DB 9; Length 28;
Best Local Similarity 73.1%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTCGGGTGG 26

Db 1 CTGGCCAGCCCAACTCTTCAGCTG 26

RESULT 2

US-09-245-802-94/c
; Sequence 94, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: U.S.A.
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/245,802
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/675,502
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05480
 FILING DATE: 18-APR-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY, ESQ., MATTHEW B.
 REGISTRATION NUMBER: 39,787
 REFERENCE/DOCKET NUMBER: 16528J-015410US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 US-09-245-802-94

Query Match 48.7%; Score 14.6; DB 10; Length 40;
 Best Local Similarity 69.0%; Pred. No. 2.4e+03;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTCGGTGGCAG 30
 DB 36 TGAGAAAGCCCGCCTTCCTCCGAAGGAG 8

RESULT 3
 US-10-093-958-22
 ; Sequence 22, Application US/10093958
 ; Publication No. US2003004423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gillies, Stephen
 ; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
 ; FILE REFERENCE: LEX-016
 ; CURRENT APPLICATION NUMBER: US/10/093,958
 ; PRIOR FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 60/274,096
 ; PRIOR FILING DATE: 2001-03-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: forward primer for gamma 1 hinge region
 US-10-093-958-22

Query Match 48.0%; Score 14.4; DB 9; Length 19;
 Best Local Similarity 93.8%; Pred. No. 3e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTCTTC 20
 DB 4 CAGAGCCCAATCTTC 19

RESULT 4
 US-09-801-274-373/c
 ; Sequence 373, Application US/09801274
 ; Patent No. US20020032319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: 2825-2009-001
 ; CURRENT APPLICATION NUMBER: US/09/801,274
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/187,510
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 60/206,129
 ; PRIOR FILING DATE: 2000-05-22
 ; NUMBER OF SEQ ID NOS: 1802
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 373
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-801-274-373

Query Match 48.0%; Score 14.4; DB 10; Length 31;
 Best Local Similarity 69.2%; Pred. No. 2.9e+03;
 Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTCTTCGGTGGCAG 30
 DB 27 CAGAGCCCACTCTTCGGTGGAG 2

RESULT 5
 US-09-733-634-11/c
 ; Sequence 11, Application US/09733634
 ; Publication No. US20030013646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Massachusetts General Hospital
 ; TITLE OF INVENTION: Method to stimulate Insulin production by pancreatic b-cells
 ; FILE REFERENCE: 17633/1240
 ; CURRENT APPLICATION NUMBER: US/09/733,634
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: US 60/170,282
 ; PRIOR FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 11
 ; LENGTH: 27
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(27)
 ; OTHER INFORMATION: Synthetic primer
 US-09-733-634-11

Query Match 46.0%; Score 13.8; DB 9; Length 27;
 Best Local Similarity 72.0%; Pred. No. 5.5e+03;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTCGGGT 25
 DB 26 CTGACAGAGCCCACTCTTCGGGT 2

RESULT 6

US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US20030060616A1
; GENERAL INFORMATION:
; APPLICANT: Sina, John E.
; Cosman, David J.
; Lupton, Stephen D.
; Mosley, Bruce A.
; Dover, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5

Query Match 46.0%; Score 13.8; DB 9; Length 46;
Best Local Similarity 88.2%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTCGCGGT 25
Db 21 GACAAACTCTTCGCGGT 37

RESULT 7
US-09-853-526-222/c
; Sequence 222, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 222
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 4-84-241
; LOCATION: 24
; OTHER INFORMATION: polymorphic base G
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-84-241.mis1
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-853-526-222

Query Match 46.0%; Score 13.8; DB 9; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCACTCTTCGCGTGGCAG 30
Db 41 AGAACTGAATTATTCACCGTGGCAG 17

RESULT 8
US-09-853-526-299/c
; Sequence 299, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 299
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens

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; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID222
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: base T ; G in SEQ ID222
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-84-241.mis1
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-853-526-299

Query Match 46.0%; Score 13.8; DB 9; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 9
US-09-901-484A-222/c
; Sequence 222, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US 09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 222
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1)..(47)
; OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID 222
; NAME/KEY: allele
; LOCATION: (24)..(24)
; OTHER INFORMATION: polymorphic base T; G in SEQ ID 222
; NAME/KEY: primer_bind
; LOCATION: (1)..(23)
; OTHER INFORMATION: potential microsequencing oligo 4-84-241.mis1
; NAME/KEY: primer_bind
; LOCATION: (25)..(47)
; OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-901-484A-299

Query Match 46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 11
US-09-820-339A-23/c
; Sequence 23, Application US/09820339A
; Patent No. US20020081652A1
; GENERAL INFORMATION:
; APPLICANT: FUCHS, Sara
; APPLICANT: BARCHAN, Dora
; APPLICANT: SOURDOUON, Miriam
; TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND TH-
; FILE REFERENCE: FUCHS=2A
; CURRENT APPLICATION NUMBER: US/09/820,339A
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 09/423,398
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: PCT/IL98/00211
US-09-901-484A-222

Query Match 46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30

```

```

Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 10
US-09-901-484A-299/c
; Sequence 299, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 299
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1)..(47)
; OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID 222
; NAME/KEY: allele
; LOCATION: (24)..(24)
; OTHER INFORMATION: polymorphic base T; G in SEQ ID 222
; NAME/KEY: primer_bind
; LOCATION: (1)..(23)
; OTHER INFORMATION: potential microsequencing oligo 4-84-241.mis1
; NAME/KEY: primer_bind
; LOCATION: (25)..(47)
; OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-901-484A-299

Query Match 46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 11
US-09-820-339A-23/c
; Sequence 23, Application US/09820339A
; Patent No. US20020081652A1
; GENERAL INFORMATION:
; APPLICANT: FUCHS, Sara
; APPLICANT: BARCHAN, Dora
; APPLICANT: SOURDOUON, Miriam
; TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND TH-
; FILE REFERENCE: FUCHS=2A
; CURRENT APPLICATION NUMBER: US/09/820,339A
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 09/423,398
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: PCT/IL98/00211

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Query Match      45.3%; Score 13.6; DB 9; Length 48;
Best Local Similarity 80.0%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  CTGACAGAGCCCAACTCTTC 20
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Db      39  CTGAAGGAGGCCAGATCTTC 20
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Search completed: June 25, 2003, 22:25:03
Job time : 92.1952 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 2545.58 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-5

Perfect score: 30
Sequence: 1 CTGACAGAGCCCACTTCGCGGTGGCAG 30

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	PCT-US97-23619-5
2	30	100.0	30	11	US-08-770-564A-5
3	24	80.0	24	9	US-08-521-634-15
4	20	66.7	20	1	PCT-US97-23619-6
5	20	66.7	20	1	PCT-US97-23619-7
6	20	66.7	20	11	US-08-770-564A-6
7	20	66.7	20	11	US-08-770-564A-7
8	18.4	61.3	25	36	US-09-956-604-105231
9	18.4	61.3	25	36	US-09-956-604A-105231
10	18.4	61.3	25	36	US-09-956-604B-105231
11	18.4	61.3	25	67	US-60-234-049-86453
12	18	60.0	48	18	US-09-404-520-39034
13	17.2	57.3	41	18	US-09-404-520-37700
14	17.2	57.3	41	79	US-60-353-790-1064
15	17	56.7	50	1	PCT-US01-47856-7470
16	17	56.7	50	40	US-10-131-831-7470
17	17	56.7	50	40	US-10-131-831-7470
18	16.8	56.0	25	17	US-09-396-196F-124326
19	16.8	56.0	25	17	US-09-396-196G-124326
20	16.4	54.7	39	18	US-09-404-520-40968
21	15.8	52.7	28	1	PCT-US02-25943-62082

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Sequence 16215, A
Sequence 16228, A
Sequence 992959, A
Sequence 187, App
Sequence 40536, A
Sequence 301573, A
Sequence 809390, A
Sequence 207601, A
Sequence 28958, A
Sequence 3806, App
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Sequence 134580, A
Sequence 592670, A
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Sequence 187, App
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Sequence 592670, A
Sequence 5017, App
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Sequence 25, Appl
Sequence 2846, App
Sequence 38072, A
Sequence 24820, A

LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 16"
PCT-US97-23619-5

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTCGCGTGGCAG 30
DB 1 CTGACAGAGCCCACTCTTCGCGTGGCAG 30

RESULT 2
US-08-770-564A-5
; Sequence 5, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-5

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTCGCGTGGCAG 30
DB 1 CTGACAGAGCCCACTCTTCGCGTGGCAG 30

RESULT 3
US-08-521-634-15/c

ALIGNMENTS

RESULT 1
PCT-US97-23619-5
; Sequence 5, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

Sequence 15, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match 80.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 GACAGAGCCCAACTCTTCGCGTG 1

RESULT 4
PCT-US97-23619-6
Sequence 6, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 16ab"
PCT-US97-23619-6

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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGACAGAGCCCAACTCTTC 20

RESULT 5
PCT-US97-23619-7
Sequence 7, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US97/23619
;; FILING DATE: Not yet assigned
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/770,564
;; FILING DATE: 20-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/770,565
;; FILING DATE: 20-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-27PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..20
;; OTHER INFORMATION: /note= "oligo 16bc"
PCT-US97-23619-7

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-576-0200
;; TELEFAX: 415-576-0300
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 7
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-7

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGCGGTGGCAG 30
Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 8

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US-09-956-604-105231/c
; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-105231

Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 9
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 10
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231
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US-08-770-564a-5.rnmp

Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 11
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          61.3%; Score 18.4; DB 67; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 12
US-09-404-520-39034/c
; Sequence 39034, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodessi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 39034
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-39034

Query Match          60.0%; Score 18; DB 18; Length 48;
Best Local Similarity 80.8%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTCGGGTGGCAG 30
Db 33 CAGAGCCCAAGCTCATGCGGCGCGCAG 8

RESULT 13
US-09-404-520-37700/c
; Sequence 37700, Application US/09404520
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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodessi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 3700
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-37700

Query Match          57.3%; Score 17.2; DB 18; Length 41;
Best Local Similarity 73.3%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGCGTGGCGAG 30
      ||||| ||||| ||||| ||||| ||||| |||||
DB      37 CGGACATAGACCAACACATGGCGCGCGCAG 8

RESULT 14
US-60-353-790-1064
; Sequence 1064, Application US/60353790
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0235 PSP
; CURRENT APPLICATION NUMBER: US/60/353,790
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3792
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1064
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-353-790-1064

Query Match          57.3%; Score 17.2; DB 79; Length 41;
Best Local Similarity 73.3%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGCGTGGCGAG 30
      ||||| ||||| ||||| ||||| ||||| |||||
DB      8  CCGTGAGAGTCCCAACTCTGCCCTGGGGCAG 37

RESULT 15
PCT-US01-47856-7470/c
; Sequence 7470, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7470
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human adenovirus type 2
PCT-US01-47856-7470

Query Match          56.7%; Score 17; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      6 AGAGCCCAACTCTTCGGCGTGGCGAG 30
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DB      31 AGAGCCCAACTCAGCGCGGTGCAG 7

Search completed: June 25, 2003, 06:20:23
Job time : 2548.19 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 21.2789 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7
Sequence: 1 GCTCAG 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	10	9	US-09-988-462-49
2	7	100.0	10	10	US-09-816-763-61
C 3	7	100.0	10	12	US-10-033-145-226
C 4	7	100.0	10	12	US-10-033-145-1449
C 5	7	100.0	11	9	US-09-249-155-34
C 6	7	100.0	13	9	US-09-879-813-84
C 7	7	100.0	13	9	US-10-146-505-84
C 8	7	100.0	13	10	US-09-770-601-4
C 9	7	100.0	13	10	US-09-770-601-6
C 10	7	100.0	14	9	US-10-146-058-41
C 11	7	100.0	15	9	US-10-146-575-21
C 12	7	100.0	15	9	US-10-145-289-2
C 13	7	100.0	15	10	US-09-922-261-10
C 14	7	100.0	16	9	US-10-146-058-39
C 15	7	100.0	17	9	US-09-879-813-51
C 16	7	100.0	17	9	US-10-041-856-79
C 17	7	100.0	17	9	US-09-780-164-249
C 18	7	100.0	17	9	US-09-780-164-250
C 19	7	100.0	17	9	US-09-780-164-612

Sequence 613, App
Sequence 738, App
Sequence 825, App
Sequence 928, App
Sequence 1066, App
Sequence 6, Appli
Sequence 7, Appli
Sequence 248, App
Sequence 249, App
Sequence 250, App
Sequence 251, App
Sequence 252, App
Sequence 253, App
Sequence 254, App
Sequence 255, App
Sequence 256, App
Sequence 257, App
Sequence 258, App
Sequence 1537, App
Sequence 1538, App
Sequence 1539, App
Sequence 1540, App
Sequence 1541, App
Sequence 1542, App
Sequence 1543, App
Sequence 1544, App

ALIGNMENTS

RESULT 1

US-09-988-462-49
Sequence 49, Application US/09988462
Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

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; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-988-462-49

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 2
US-09-816-763-61
; Sequence 61, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: ISGF3
US-09-816-763-61

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 1 GCTTCAG 7

RESULT 3
US-10-033-145-226/c
; Sequence 226, Application US/10033145
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS

```


; SEQ ID NO 34
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-34

Query Match 100.0%; Score 7; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 10 GCTTCAG 4

RESULT 6

US-09-879-813-84/c
; Sequence 84, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-09-879-813-84

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 7 GCTTCAG 1

RESULT 7

US-10-146-505-84/c
; Sequence 84, Application US/10146505
; Publication No. US20030108889A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-10-146-505-84

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 7 GCTTCAG 1

RESULT 8

US-09-770-601-4
; Sequence 4, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/127,276
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/054,730
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-770-601-4

Query Match 100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 7 GCTTCAG 13

RESULT 9

US-09-770-601-6/c
; Sequence 6, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26

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; PRIOR APPLICATION NUMBER: 09/127,276
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/054,730
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-770-601-6

Query Match      100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 7 GCTTCAG 1

RESULT 10
US-10-146-058-41/c
; Sequence 41, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-41

Query Match      100.0%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 11 GCTTCAG 5

RESULT 11
US-10-146-575-21/c
; Sequence 21, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-146-575-21

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 8 GCTTCAG 2

RESULT 12
US-10-145-289-2
; Sequence 2, Application US/10145289
; Publication No. US20030077812A1
; GENERAL INFORMATION:
; APPLICANT: James G. McArthur
; APPLICANT: Dale John Talbot
; APPLICANT: Andrew D. Simmons
; APPLICANT: Ryan McGuinness
; APPLICANT: Michael Kelly
; APPLICANT: Lisa V. Tsui
; APPLICANT: Thomas Dull
; TITLE OF INVENTION: LENTIVIRAL VECTORS ENCODING CLOTTING
; FILE REFERENCE: 131.2USU1
; CURRENT APPLICATION NUMBER: US/10/145,289
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/291,083
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-289-2
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Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      9 GCTTCAG 15

RESULT 13
US-09-922-261-10/c
; Sequence 10, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 1001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-261-10

Query Match      100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db     11 GCTTCAG 5

RESULT 14
US-10-146-058-39/c
; Sequence 39, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
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CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202)393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-39

Query Match      100.0%; Score 7; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      7 GCTTCAG 1

RESULT 15
US-09-879-813-51/c
; Sequence 51, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(12)
; OTHER INFORMATION: D3
; OTHER INFORMATION: The sequence GACCC between positions 7 and 12 replace the sequence
; OTHER INFORMATION: e AGGACTGT
US-09-879-813-51

Query Match      100.0%; Score 7; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      7 GCTTCAG 7
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Db 17 GCTTCAG 11

Search completed: June 25, 2003, 22:25:08
Job time : 21.2789 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 22.7689 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15

Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
- 1: /cgn2_6/prodata/2/ina/5A-COMB.seq.*
 - 2: /cgn2_6/prodata/2/ina/5B-COMB.seq.*
 - 3: /cgn2_6/prodata/2/ina/6A-COMB.seq.*
 - 4: /cgn2_6/prodata/2/ina/6B-COMB.seq.*
 - 5: /cgn2_6/prodata/2/ina/PTUS-COMB.seq.*
 - 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	2	US-08-770-565-10
2	15	100.0	19	2	US-08-770-565-9
3	15	100.0	26	1	US-08-330-123A-23
4	15	100.0	26	1	US-08-482-115B-23
5	15	100.0	26	2	US-08-660-678A-23
6	15	100.0	26	2	US-08-710-249-26
7	15	100.0	26	2	US-08-485-778-19
8	15	100.0	26	2	US-08-472-802C-24
9	15	100.0	26	3	US-08-520-550A-19
10	15	100.0	26	3	US-08-998-443-23
11	15	100.0	26	4	US-08-974-549A-598
12	15	100.0	26	4	US-09-060-523-23
13	15	100.0	26	4	US-09-220-157A-26
14	15	100.0	26	4	US-09-286-959B-4
15	15	100.0	26	4	US-09-580-517-23
16	15	100.0	27	2	US-08-770-565-26
17	15	100.0	30	2	US-08-770-565-8
18	14	93.3	27	3	US-08-630-172-24
19	14	93.3	27	4	US-09-375-419-24
20	14	93.3	30	2	US-08-833-377-6
21	13.4	89.3	18	4	US-08-974-549A-543
22	12.4	82.7	23	4	US-09-273-839A-3
23	12.4	82.7	26	1	US-08-480-604A-16
24	12.4	82.7	26	2	US-08-405-496A-16
25	12.4	82.7	26	4	US-08-915-136-16
26	12.4	82.7	26	4	US-08-957-310-16
27	12.4	82.7	33	3	US-08-630-172-22

28	12.4	82.7	33	4	US-09-375-419-22	Sequence 22, Appl
29	12.4	82.7	40	1	US-08-395-800A-12	Sequence 12, Appl
30	12.4	82.7	42	1	US-08-439-813-2	Sequence 2, Appl
31	12.4	82.7	42	5	PCT-US96-05291A-2	Sequence 2, Appl
32	12	80.0	30	1	US-08-349-006-3	Sequence 3, Appl
33	12	80.0	30	5	PCT-US94-02107-3	Sequence 3, Appl
34	11.8	78.7	24	2	US-09-258-257-3	Sequence 3, Appl
35	11.8	78.7	24	2	US-09-258-371-3	Sequence 3, Appl
36	11.8	78.7	24	3	US-08-569-721A-3	Sequence 3, Appl
37	11.8	78.7	24	3	US-08-751-230-3	Sequence 3, Appl
38	11.8	78.7	24	3	US-09-499-082-3	Sequence 3, Appl
39	11.8	78.7	24	4	US-09-258-372-3	Sequence 3, Appl
c 40	11.8	78.7	26	2	US-09-258-257-4	Sequence 4, Appl
c 41	11.8	78.7	26	3	US-09-258-371-4	Sequence 4, Appl
c 42	11.8	78.7	26	3	US-08-569-721A-4	Sequence 4, Appl
c 43	11.8	78.7	26	3	US-08-751-230-4	Sequence 4, Appl
c 44	11.8	78.7	26	3	US-09-499-082-4	Sequence 4, Appl
c 45	11.8	78.7	26	4	US-09-258-372-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
; Sequence 10, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-10

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 GCTCTAGATGAACG 15

Db
1 GCTCTAGAAATGAACG 15

RESULT 2

```

US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565

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APPLICATION NUMBER: US/08/770,565-9
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Stella, John R.
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 415-576-0300
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-770-565-9

Query Match 100.0%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 15: Conservative 0; Mismatches 0; Indels

Qy 1 GCTCTAGAAATGAACG 15
|||
Db 1 GCTCTAGAAATGAACG 15
|||

RESULT 3

US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match	100.0%;	Score 15;	DB 1;	Length 26;
Best Local Similarity	100.0%;	Pred. No. 8;		
Matches	15:	Conservative	0:	Mismatches
			0:	Indels

QY 1 GCTCTAGAATGAACG 15
|||
db 5 GCTCTAGAATGAACG 19
|||

RESULT 4

US-08-482-115B-23
 ; Sequence 23, Application US/08482115B
 ; Patent No. 5776679
 ; GENERAL INFORMATION:
 ; APPLICANT: Willleponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Assays for the RNA Component of Human
 ; TITLE OF INVENTION: Telomerase
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,115B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/330,123

;; FILING DATE: 27-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-000830US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 5
US-08-660-678A-23
; Sequence 23, Application US/08560678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-660-678A-23

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 6
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 7
US-08-485-778-19
; Sequence 19, Application US/08485778

```
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 9
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995

Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 8
US-08-472-802C-24
Sequence 24, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
```



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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-9540
; TELEFAX: 617-861-6240
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550A-19

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 10
US-08-998-443-23
; Sequence 23, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-998-443-23

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11
US-08-974-549A-598
; Sequence 598, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
|||||
Db 5 GCTCTAGATGAACG 19

RESULT 12
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
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Db 5 GCTCTAGATGAACG 19

RESULT 13
US-09-220-157A-26
Sequence 26, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 14

US-09-286-959B-4
Sequence 4, Application US/09286959B
Patent No. 6300131
GENERAL INFORMATION:
APPLICANT: Johns Hopkins University
APPLICANT: Greider, Carol W.

APPLICANT: Le, Siyuan
TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
FILE REFERENCE: 07265/157001
CURRENT APPLICATION NUMBER: US/09/286,959B
CURRENT FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,783
PRIOR FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 26

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 15

US-09-580-517-23
Sequence 23, Application US/09580517
Patent No. 6320039
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
FENG, Junli
FUNK, Walter

ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

Search completed: June 25, 2003, 00:24:39
Job time : 22.7689 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 773.367 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO NUC
Gapex 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	10	66.7	49	17	BH791685
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c 11	9	60.0	28	17	TA116E03P
c 12	9	60.0	30	9	AU257604
c 13	9	60.0	31	9	A1032592
c 14	9	60.0	34	12	BG339578
c 15	9	60.0	34	12	BG340055
c 16	9	60.0	36	12	BE797241
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c 18	9	60.0	38	17	AZ786040
c 19	9	60.0	40	12	BG563012
c 20	9	60.0	41	9	AU258962
c 21	9	60.0	41	17	AZ775318
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c 35	9	60.0	46	17	TA114E02P
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c 39	9	60.0	50	9	AU105700
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c 43	8	53.3	19	17	AZ309082
c 44	8	53.3	19	17	AZ659092
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AZ471573 F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286G13 F, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ471573 19 bp DNA linear GSS 04-OCT-2000
1M0286G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286G13 F, DNA sequence.
AZ471573
GSS
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0286 row: G column: 13
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286G13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 3 c 6 g 4 t
 ORIGIN
 Query Match 66.7%; Score 10; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 CTCTAGAATG 11
 |||||
 Db 15 CTCTAGAATG 6

RESULT 2
 TA264G10Q 29 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 264g10, reverse sequence, genomic survey sequence.
 ACCESSION AL487013
 VERSION AL487013.1 GI:11850630
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 29)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Title Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Comment Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
 1. .29
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="264g10"

BASE COUNT 11 a 5 c 11 g 2 t
 ORIGIN

Query Match 66.7%; Score 10; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 AGAATGAACG 15
 |||||
 Db 7 AGAATGAACG 16

RESULT 3
 AV964763/c 34 bp mRNA linear EST 14-MAR-2002
 LOCUS
 DEFINITION AV964763 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad1506 5', mRNA sequence.
 ACCESSION AV964763
 VERSION AV964763.1 GI:19454459
 KEYWORDS EST.
 SOURCE Ciona intestinalis.
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 34)
 Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
 TITLE Expressed genes in Ciona intestinalis
 JOURNAL Unpublished (2000)
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 Source
 1. .34
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciad1506"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult"
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT 12 a 5 c 8 g 9 t
 ORIGIN

Query Match 66.7%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAAT 10
 |||||
 Db 16 GCTCTAGAAT 7

RESULT 4
 BH791685 49 bp DNA linear GSS 02-APR-2002
 LOCUS
 DEFINITION BH791685 SALK 060837.45.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_060837.45.60.x, DNA sequence.

ACCESSION BH791685
 VERSION BH791685.1 GI:19885809
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 49)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.

FEATURES

source
 1. .49
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_060837.45.60.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 15 a 9 c 9 g 16 t

Query Match 66.7%; Score 10; DB 17; Length 49;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAAT 10
 |||||
 Db 39 GCTCTAGAAAT 48

RESULT 5
 AU259636
 LOCUS AU259636 3'-directed mouse cDNA library Mus musculus cDNA clone
 DEFINITION BED0015510 3', mRNA sequence.

ACCESSION AU259636
 VERSION AU259636.1 GI:20326342
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Kato, K. and Matoba, R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkato@bs.aist-nara.ac.jp.

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.
 Location/Qualifiers
 1. .22

source
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BED0015510"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue type="brain"
 /note="Vector: pGEM-T-easy"
 13 a 3 c 4 g 2 t

Query Match 60.0%; Score 9; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAATGAAC 14
 |||||
 Db 11 AGAATGAAC 19

RESULT 6
 AU259636
 LOCUS AU259636 25 bp mRNA linear EST 21-DEC-1999
 DEFINITION wi55d06.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:2394155 3', similar to TR:O75053 KIAA0465 PROTEIN ;, mRNA sequence.
 ACCESSION AU259636
 VERSION AU259636.1 GI:5179013
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1675 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .25

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2394155"
 /clone_lib="NCI CGAP Co16"
 /tissue type="colon tumor, RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Co10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaldo.
 9 a 3 c 7 g 6 t

BASE COUNT
 ORIGIN

Query Match 60.0%; Score 9; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTAGATGA 12
 |||||
 Db 12 CTAGATGA 20

RESULT 7
 AU254302/c
 LOCUS AU254302 27 bp mRNA linear EST 25-APR-2002
 DEFINITION BED0001498 3', mRNA sequence.
 ACCESSION AU254302
 VERSION AU254302.1 GI:20315955
 KEYWORDS house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Kato, K. and Macoba, R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kikuva Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatob@bs.aist-nara.ac.jp,
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BED0001498"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEM-T-easy"
 BASE COUNT 11 a 3 c 4 g 9 t
 ORIGIN

Query Match 60.0%; Score 9; DB 9; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TAGAATGAA 13
 |||||
 Db 25 TAGAATGAA 17

RESULT 8
 BH812447
 LOCUS BH812447 27 bp DNA linear GSS 02-MAY-2002
 DEFINITION SALK_061781 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061781, DNA sequence.

ACCESSION BH812447
 VERSION BH812447.1 GI:20390902
 KEYWORDS GSS.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_061781"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 12 a 3 c 5 g 7 t
 ORIGIN

Query Match 60.0%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTAGAT 10
 |||||
 Db 18 CTCTAGAT 26

RESULT 9
 BH849811
 LOCUS BH849811 27 bp DNA linear GSS 13-JUN-2002
 DEFINITION SALK_070310.38.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_070310.38.90.x, DNA sequence.

ACCESSION BH849811
 VERSION BH849811.1 GI:21420682
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_070310.38.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
ORIGIN

7 a 2 c 8 g 10 t

Query Match 60.0%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATG 11
|||||
Db 8 TCTAGATG 16

RESULT 10
TA349B02P 27 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 349b02, forward sequence,
genomic survey sequence.

ACCESSION AL493641

VERSION AL493641.1 GI:11869420

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 27)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .27
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="349b02"

BASE COUNT 4 a 10 c 8 g 5 t

Query Match 60.0%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAA 9
|||||
Db 7 GCTCTAGAA 15

RESULT 11
TAL16E03P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 116e03, forward sequence,
genomic survey sequence.

ACCESSION AL462526

VERSION

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 28)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .28
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="116e03"

BASE COUNT 7 a 5 c 8 g 8 t

ORIGIN

Query Match 60.0%; Score 9; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAATGAACG 15
|||||
Db 2 GAATGAACG 10

RESULT 12

AU257604

LOCUS

DEFINITION AU257604 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0011024 3', mRNA sequence.

ACCESSION AU257604.1 GI:20322387

VERSION AU257604

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS Kato, K. and Matoba, R.

TITLE Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished (2002)

COMMENT Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@bs.aist-nara.ac.jp

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1. .30
/organism="Mus musculus"
/db_xref="taxon:10090"

```

/clone="BED0011024"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/notes="Vector: pGEN-T-easy"
BASE COUNT      13 a      6 c      4 g      7 t
ORIGIN

Query Match      60.0%; Score 9; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTCTAGAT 10
      |||||
Db      5 CTCTAGAT 13

RESULT 13
AI032592/c
LOCUS
DEFINITION      ow73q08.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA
clone IMAGE:1652510 3' similar to TR:015102 O15102 HYPOTHETICAL
40.0 KD PROTEIN. 1; mRNA sequence.
ACCESSION      AI032592
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 31)
AUTHORS
TITLE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL
COMMENT      Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. Ef from Amerisham
High quality sequence stop: 1.
FEATURES
source
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1652510"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bernaldo."
BASE COUNT      5 a      10 c      6 g      10 t
ORIGIN

Query Match      60.0%; Score 9; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TCTAGATG 11
      |||||
Db      28 TCTAGATG 20

RESULT 14
BG339578
LOCUS
DEFINITION      34 bp mRNA linear EST-27-FEB-2001
602437433F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:455280 5',
mRNA sequence.
ACCESSION      BG339578
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 34)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1256 row: a column: 09
High quality sequence stop: 34.
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:455280"
/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      14 a      9 c      9 g      2 t
ORIGIN

Query Match      60.0%; Score 9; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGAATGAAC 14
      |||||
Db      5 AGAATGAAC 13

RESULT 15
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LOCUS
DEFINITION      34 bp mRNA linear EST-27-FEB-2001
602438218F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4556092 5',
mRNA sequence.
ACCESSION      BG340055
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 34)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1258 row: c column: 05
High quality sequence stop: 34.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4556092"
/clone_lib="NIH MGC 46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 14 a 9 c 9 g 2 t

ORIGIN

Query Match 60.0%; Score 9; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAC 14

Db 5 AGAATGAC 13

Search completed: June 23, 2003, 10:10:27
Job time : 774.52 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 658.446 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTTAGAATGAACG 15

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*

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- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
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- 8: /cgn2_6/ptodata/1/pna/US13_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US17_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15	100.0	21	1	PCT-US03-04088-543
C 3	15	100.0	21	1	PCT-US03-04088-547
C 4	15	100.0	21	1	PCT-US03-04088-551
C 5	15	100.0	21	1	PCT-US03-04088-555
C 6	15	100.0	21	1	PCT-US03-04088-559
C 7	15	100.0	21	1	PCT-US03-04088-563
C 8	15	100.0	21	1	PCT-US03-04088-567
C 9	15	100.0	26	9	US-09-721-456-598
C 10	15	100.0	26	9	US-10-325-810-598
C 11	15	100.0	26	9	US-10-325-810-598
C 12	15	100.0	26	9	US-10-325-810-598
C 13	15	100.0	30	10	US-10-330-872-5
C 14	14	93.3	23	9	US-10-310-188-36216
C 15	14	93.3	25	12	US-60-427-808-952738
C 16	14	93.3	25	13	US-60-469-545-13722
C 17	14	93.3	25	13	US-60-469-545-13722
C 18	13	86.7	18	6	US-09-721-456-543
C 19	13	86.7	18	9	US-10-325-810-543
C 20	13	86.7	21	1	PCT-US03-04088-538

21	13	86.7	21	1	PCT-US03-04088-542	Sequence 542, App
C 22	13	86.7	21	1	PCT-US03-04088-546	Sequence 546, App
C 23	13	86.7	21	1	PCT-US03-04088-550	Sequence 550, App
C 24	13	86.7	21	1	PCT-US03-04088-554	Sequence 554, App
C 25	13	86.7	21	1	PCT-US03-04088-558	Sequence 558, App
C 26	13	86.7	25	6	US-09-660-222-3845	Sequence 3845, App
C 27	13	86.7	25	6	US-09-660-222-3846	Sequence 3846, App
C 28	13	86.7	25	6	US-09-660-222-3854	Sequence 3854, App
C 29	13	86.7	25	9	US-10-098-263B-118949	Sequence 118949, App
C 30	13	86.7	25	9	US-10-355-577-173196	Sequence 173196, App
C 31	13	86.7	25	12	US-60-427-808-738286	Sequence 738286, App
C 32	13	86.7	25	12	US-60-427-808-738286	Sequence 738286, App
C 33	12	80.0	25	7	US-09-954-445A-17344	Sequence 17344, App
C 34	12	80.0	25	7	US-09-954-445A-17345	Sequence 17345, App
C 35	12	80.0	25	7	US-09-954-445A-17346	Sequence 17346, App
C 36	12	80.0	25	7	US-09-954-445A-17347	Sequence 17347, App
C 37	12	80.0	25	7	US-09-954-445A-17348	Sequence 17348, App
C 38	12	80.0	25	9	US-10-098-263B-64498	Sequence 64498, App
C 39	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 40	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 41	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 42	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
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C 44	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 45	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App

ALIGNMENTS

RESULT 1
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; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0% Score 15; DB 1; Length 21;

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PCT-US03-04088-547
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 547
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(2)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(5)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(9)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(14)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-547
Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCTAGATGAACG 15
Dd 19 GCCTAGATGAACG 5
RESULT 4
PCT-US03-04088-551
Sequence 551, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

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; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
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; OTHER INFORMATION: antisense region
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; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
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; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
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; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; PCT-US03-04088-551

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 1 GCUCUAGAAUGAACG 15

RESULT 5
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; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
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; FEATURE:
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; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
PCT-US03-04088-555
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Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 GCTCTAGAATGAACG 15
Db 19 GCTCTAGAATGAACG 5
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RESULT 6
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; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(9)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
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; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; OTHER INFORMATION: 3'-Internucleotide Linkage
PCT-US03-04088-559
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Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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OY 1 GCTCTAGAATGAACG 15
Db 1 GCUCUAGAAGACG 15
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RESULT 7
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-520
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Query Match 100.0%; Score 15; DB 1; Length 23;
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 23 GCTCTAGAAATGAACG 9

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
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; PRIOR FILING DATE: 2002-08-29
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; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 23
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

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Db 21 GCTCTAGAAATGAACG 7

RESULT 9
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; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Haxley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

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; Morin, Gregg B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
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; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

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Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 GCTCTAGAATGAACG 19

RESULT 11

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; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; Funk, Junli
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23

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Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 GCTCTAGAATGAACG 19

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RESULT 12
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C

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; CURRENT APPLICATION NUMBER: US/10/330,872
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GCTCTAGAATGAACG 15

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US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match          100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 35;
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; Sequence 36216, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
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; SEQ ID NO 36216
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-36216

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; Sequence 952738, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Title: US-08-770-564A-10

Perfect score: 15

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6	15	100.0	25	25	US-09-642-177-4
7	15	100.0	26	1	PCT-US96-14679-27
8	15	100.0	26	1	PCT-US96-14679A-27
9	15	100.0	26	1	PCT-US99-03302-4
10	15	100.0	26	1	PCT-US99-07533-4
11	15	100.0	26	1	PCT-US99-07533-4
12	15	100.0	26	6	US-08-272-102-23
13	15	100.0	26	7	US-08-387-524-19
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17	15	100.0	26	9	US-08-520-550-19
18	15	100.0	26	9	US-08-521-634-41
19	15	100.0	26	10	US-08-660-678-23
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21	15	100.0	26	13	US-08-911-312A-23

Sequence 312, App
Sequence 17, Appl
Sequence 598, App
Sequence 23, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 45, Appl
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Sequence 598, App
Sequence 598, App
Sequence 5, Appl
Sequence 598, App
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Sequence 9, Appl
Sequence 26, Appl
Sequence 312, App
Sequence 312, App
Sequence 26, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 5, Appl

LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..15
OTHER INFORMATION: /note= "oligo 21ab3"

PCT-US97-23619-10

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATGACG 15

RESULT 2

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; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-10

Query Match 100.0%; Score 15; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACG 15
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Db 1 GCTCTAGATGACG 15

RESULT 3

PCT-US97-23619-9

Sequence 312, App
Sequence 17, Appl
Sequence 598, App
Sequence 23, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 45, Appl
Sequence 598, App
Sequence 598, App
Sequence 598, App
Sequence 5, Appl
Sequence 598, App
Sequence 598, App
Sequence 9, Appl
Sequence 26, Appl
Sequence 312, App
Sequence 312, App
Sequence 26, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 5, Appl

Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

Sequence 9, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note= "oligo 21ab"
PCT-US97-23619-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
Db 1 GCTCTAGAAATGAACG 15
RESULT 4
US-08-770-564A-9
Sequence 9, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
Db 1 GCTCTAGAAATGAACG 15
RESULT 5
US-09-250-336A-4
Sequence 4, Application US/09250336A
GENERAL INFORMATION:
APPLICANT: STROVEL, Jeffrey W.
APPLICANT: STAMBERG, Judith
APPLICANT: ABRUZZO, Lynne V.
APPLICANT: HIGHSMITH, Edward
TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
FILE REFERENCE: 10460-4 (210460.0004)
CURRENT APPLICATION NUMBER: US/09/250,336A
CURRENT FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: US 60/074,793
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: PCT/US99/03302
PRIOR FILING DATE: 1999-02-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4
Query Match 100.0%; Score 15; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
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Db 4 GCTCTAGATGAACG 18

RESULT 6

US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: R3c, Primer
US-09-642-177-4

Query Match 100.0%; Score 15; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 4 GCTCTAGATGAACG 18

RESULT 7

PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779

TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 8

PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 9

PCT-US99-03302-4


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; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; FILE REFERENCE: 1489JS 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 10
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 11
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
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; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 12
US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272.102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William W
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 13
US-08-387-524-19
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; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-524-19

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Query Match 100.0%; Score 15; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

```

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RESULT 14
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

```

```

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802A-24

```

```

Query Match 100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

```

```

RESULT 15
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802B-24

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Query Match      100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
        |||||
Db       5 GCTCTAGATGAACG 19

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Job time : 1258.16 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 120.538 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	26	9	US-10-044-692-312 Sequence 312, App
2	15	100.0	26	9	US-10-044-539-312 Sequence 312, App
3	15	100.0	26	10	US-09-057-351-23 Sequence 23, Appl
4	13	86.7	25	9	US-10-098-263B-118949 Sequence 118949
5	13	86.7	26	9	US-09-952-522B-19 Sequence 19, Appl
6	13	86.7	28	10	US-09-844-006A-3 Sequence 3, Appl
7	12	80.0	23	9	US-09-952-522B-17 Sequence 17, Appl
8	12	80.0	23	9	US-09-952-522B-31 Sequence 31, Appl
9	12	80.0	25	9	US-10-215-112-6862 Sequence 6862, Ap
10	12	80.0	25	9	US-10-098-263B-64498 Sequence 64498, A
11	12	80.0	26	9	US-10-011-366-16 Sequence 16, Appl
12	11	73.3	21	9	US-09-997-868-13 Sequence 13, Appl
13	11	73.3	22	10	US-09-765-873A-5 Sequence 5, Appl
14	11	73.3	23	9	US-09-952-522B-9 Sequence 9, Appl
15	11	73.3	24	9	US-10-245-813-2 Sequence 2, Appl
16	11	73.3	25	9	US-10-098-263B-10750 Sequence 10750, A
17	11	73.3	25	9	US-10-098-263B-33532 Sequence 33532, A
18	11	73.3	25	9	US-10-098-263B-44593 Sequence 44593, A
19	11	73.3	25	9	US-10-098-263B-44594 Sequence 44594, A

Sequence 104702, Sequence 11, Appl
Sequence 13, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 40, Appl
Sequence 12, Appl
Sequence 7, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 2, Appl
Sequence 49, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 1399, Ap
Sequence 5826, Ap
Sequence 8894, Ap
Sequence 60549, A
Sequence 63103, A

25 9 US-10-098-263B-104702
26 9 US-10-118-495-11
26 9 US-10-118-495-13
27 10 US-09-784-508-8
27 10 US-10-162-223-2
29 10 US-09-985-983-40
31 10 US-09-848-616-12
33 9 US-09-964-895-7
33 9 US-09-964-895-15
34 10 US-09-784-508-10
36 9 US-10-166-183-14
36 9 US-10-127-816-18
36 10 US-09-784-508-11
21 8 US-08-913-322-3
21 10 US-09-767-479-15
22 9 US-09-981-648-11
22 9 US-09-989-708-2
23 9 US-10-071-485-49
23 10 US-09-911-176B-24
24 9 US-10-180-762-24
24 9 US-10-241-258-24
25 9 US-10-098-263B-1399
25 9 US-10-098-263B-5826
25 9 US-10-098-263B-8894
25 9 US-10-098-263B-60549
25 9 US-10-098-263B-63103

ALIGNMENTS

RESULT 1

US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 2
US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
```

```

; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
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TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 15; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 5 GCTCTAGAAATGAACG 19

RESULT 4

US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match 86.7%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 82; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TCTAGAAATGAACG 8

RESULT 5

US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lluil, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone sialoprotein forward primer

US-09-952-522B-19

Query Match 86.7%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 82; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 13
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCTCTAGAAATGAACG 13

RESULT 6

US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; LOCATION: (1)..(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match 86.7%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 82; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 13
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCTCTAGAAATGAACG 13

RESULT 7

US-09-952-522B-17
; Sequence 17, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lluil, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 23

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
; OTHER INFORMATION: forward primer
US-09-952-522B-17

Query Match      80.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
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Db      1 GCTCTAGAATGA 12

RESULT 8
US-09-952-522B-31
; Sequence 31, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
; OTHER INFORMATION: forward primer
US-09-952-522B-31

Query Match      80.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
      |||||
Db      1 GCTCTAGAATGA 12

RESULT 9
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6862
; LENGTH: 25

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-10-215-112-6862

Query Match      80.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
      |||||
Db      15 GCTCTAGAATGA 4

RESULT 10
US-10-098-263B-64498/c
; Sequence 64498, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match      80.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TCTAGAATGAAC 14
      |||||
Db      23 TCTAGAATGAAC 12

RESULT 11
US-10-011-366-16
; Sequence 16, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/011,366
; APPLICATION NUMBER: US/10/011,366
; FILING DATE: 16-No. US20030054493A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,310

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FILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 08/329,154
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match 80.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
|||||
DB 1 GCTCTAGATGA 12

RESULT 12
US-09-997-868-13/c
Sequence 13, Application US/09997868
Publication No. US20030031654A1
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/997,868
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match 73.3%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 11 GCTCTAGATG 1

RESULT 13
US-09-765-873A-5
Sequence 5, Application US/09765873A
Patent No. US20010053847A1
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: primer
US-09-765-873A-5

Query Match 73.3%; Score 11; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 3 GCTCTAGATG 13

RESULT 14
US-09-952-522B-9
Sequence 9, Application US/09952522B
Publication No. US20030082152A1
GENERAL INFORMATION:
APPLICANT: Katz, Adam J.
APPLICANT: Lull, Ramon
APPLICANT: Putrell, J. William
APPLICANT: Hedrick, Marc H.
APPLICANT: Benhaim, Prosper
APPLICANT: Lorenz, Hermann Peter
APPLICANT: Zhu, Min
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
FILE REFERENCE: 30448.77US11
CURRENT APPLICATION NUMBER: US/09/952,522B
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US00/06232
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/123,711
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/162,462
PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: osteocalcin forward primer
US-09-952-522B-9

Query Match 73.3%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGAATG 11
| | | | | | | | | |
Db 1 GCTCTAGAATG 11

RESULT 15
US-10-245-813-2
; Sequence 2, Application US/10245813
; Publication No. US2003060443A1
; GENERAL INFORMATION:
; APPLICANT: Gyun Min Lee
; APPLICANT: No. US2003060443A1Soo Kim
; TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE
; TITLE OF INVENTION: EXPRESSION OF ANTISENSE RNA OF CASPASE-2
; FILE REFERENCE: 118.19-US-01
; CURRENT APPLICATION NUMBER: US/10/245,813
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 2001-57353
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: casp3L primer
US-10-245-813-2

Query Match 73.3%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGAATG 11
| | | | | | | | | |
Db 1 GCTCTAGAATG 11

Search completed: June 23, 2003, 20:01:32
Job time : 120.538 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 23.4861 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-10
Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	2	US-08-770-565-10
2	15	100.0	19	2	US-08-770-565-9
3	15	100.0	26	1	US-08-330-123A-23
4	15	100.0	26	1	US-08-482-115B-23
5	15	100.0	26	2	US-08-660-678A-23
6	15	100.0	26	2	US-08-710-249-26
7	15	100.0	26	2	US-08-485-778-19
8	15	100.0	26	2	US-08-472-802C-24
9	15	100.0	26	3	US-08-520-550A-19
10	15	100.0	26	3	US-08-998-443-23
11	15	100.0	26	4	US-08-974-549A-598
12	15	100.0	26	4	US-09-060-523-23
13	15	100.0	26	4	US-09-220-157A-26
14	15	100.0	26	4	US-09-286-959B-4
15	15	100.0	26	4	US-09-580-517-23
16	15	100.0	27	2	US-08-770-565-26
17	15	100.0	30	2	US-08-770-565-8
18	14	93.3	27	3	US-08-630-172-24
19	14	93.3	27	4	US-09-375-419-24
20	14	93.3	30	2	US-08-833-377-6
21	13	86.7	18	4	US-08-974-549A-543
22	12	80.0	26	1	US-08-480-604A-16
23	12	80.0	26	2	US-08-405-496A-16
24	12	80.0	26	4	US-08-915-136-16
25	12	80.0	26	4	US-08-957-310-16
26	12	80.0	30	1	US-08-349-006-3
27	12	80.0	30	5	PCT-US94-02107-3

28	12	80.0	33	3	US-08-630-172-22	Sequence 22, Appl
29	12	80.0	33	4	US-09-375-419-22	Sequence 22, Appl
30	11	73.3	11	2	US-08-770-565-11	Sequence 11, Appl
C 31	11	73.3	21	4	US-08-026-143B-13	Sequence 13, Appl
C 32	11	73.3	21	5	PCT-US92-10621-13	Sequence 13, Appl
C 33	11	73.3	21	5	PCT-US94-02233-13	Sequence 13, Appl
34	11	73.3	22	4	US-08-627-216A-5	Sequence 5, Appl
35	11	73.3	23	3	US-08-973-068-46	Sequence 46, Appl
36	11	73.3	26	4	US-09-153-310-4	Sequence 4, Appl
37	11	73.3	30	2	US-08-995-927-7	Sequence 7, Appl
38	11	73.3	30	4	US-09-349-627-5	Sequence 5, Appl
39	11	73.3	30	4	US-09-582-096-7	Sequence 7, Appl
40	11	73.3	37	1	US-08-591-492-17	Sequence 17, Appl
41	11	73.3	37	3	US-08-815-190A-3	Sequence 3, Appl
42	11	73.3	39	4	US-09-091-305-3	Sequence 3, Appl
43	11	73.3	40	1	US-08-395-800A-12	Sequence 12, Appl
C 44	11	73.3	46	1	US-08-399-696-14	Sequence 14, Appl
C 45	10	66.7	15	2	US-08-624-601-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
; Sequence 10, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-10

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15

Db 1 GCTCTAGATGAACG 15

RESULT 2
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15

RESULT 3
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTIEU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 4
US-08-482-115B-23
; Sequence 23, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTIEU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123

;; FILING DATE: 27-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-000830US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 5
US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-660-678A-23

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 6
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 7
US-08-485-778-19
; Sequence 19, Application US/08485778

Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 8
US-08-472-802C-24
Sequence 24, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 9
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 19:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-19

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 10
US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 11
US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 12
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 13
US-09-220-157A-26
Sequence 26, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single


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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 14
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 15
US-09-580-517-23
; Sequence 23, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
; FILING DATE: 25-May-2000
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,123
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

Search completed: June 23, 2003, 10:17:07
Job time : 23.4861 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 99.6813 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAV41177	RNA component of h
2	15	100.0	19	AAV41176	RNA component of h
3	15	100.0	25	AAZ08704	Human telomerase R
4	15	100.0	26	AAT10304	RNA component of h
5	15	100.0	26	AAT10299	RNA component of h
6	15	100.0	26	AAT11044	Primer for product
7	15	100.0	26	AAT58811	Human telomerase P
8	15	100.0	26	AAV19489	Human htr gene tr
9	15	100.0	26	AAV17033	Telomerase PCR pri

10	15	100.0	26	20	AAZ08788	Human telomerase R
11	15	100.0	26	20	AAZ77402	Human telomerase R
12	15	100.0	26	20	AAZ01542	PCR primer for Hum
13	15	100.0	26	21	AAZ88250	Human telomerase R
14	15	100.0	26	24	ABK48024	Human telomerase-a
15	15	100.0	26	24	AAD24246	Human telomerase (
16	15	100.0	27	19	AAV41193	RNA component of h
17	15	100.0	27	24	AAZ95497	Human telomerase R
18	15	100.0	30	19	AAV63649	Antisense oligonuc
19	15	100.0	30	19	AAV41175	RNA component of h
20	15	100.0	30	20	AZ223631	Human clone 28-1 t
21	15	100.0	30	22	AAZ03476	Antisense oligonuc
22	15	100.0	30	23	AAZ15928	Human telomerase p
23	15	100.0	30	24	ABA91517	Oligonucleotide us
24	14	93.3	27	18	AAT97049	Sense primer for h
25	13	86.7	13	23	AAZ15930	Human telomerase p
26	13	86.7	28	24	ABA04366	CRT C-domain-green
27	13	86.7	32	21	AAA46113	Human GPCR TDAG8(I
28	12	80.0	17	22	AAF57369	Murine Cdc25A intr
29	12	80.0	26	17	AAT29258	C. difficile toxin
30	12	80.0	26	19	AAV30567	Clostridium diffi
31	12	80.0	26	21	ABK09963	Novel recombinant
32	12	80.0	30	15	AAQ71630	HCMV IE-exon-4 sub
33	12	80.0	33	18	AAT97047	Sense primer for h
34	12	80.0	39	22	AAF81502	Novel human G prot
35	12	80.0	39	22	AAF87602	RNA associated wit
36	11	73.3	11	19	AAV41178	RNA component of h
37	11	73.3	11	23	AAZ15929	Human telomerase p
38	11	73.3	19	22	AAH43421	IS3 reverse prime
39	11	73.3	21	14	AAQ43258	Sequence encoding
40	11	73.3	21	14	AAQ43257	Sequence encoding
41	11	73.3	21	15	AAQ71457	Rx 2.4 prorelaxin
42	11	73.3	22	24	AAD33073	Phenylalanine ammo
43	11	73.3	22	24	AAD26921	Rhodospiridium tor
44	11	73.3	23	18	AAT49421	Banana bunchy top
45	11	73.3	24	19	AAV43976	C. sativa chloropl

ALIGNMENTS

RESULT 1
AAV41177
ID AAV41177 standard; DNA; 15 BP.
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AC AAV41177;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 21ab3.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX
DR WPI; 1998-377670/32.

XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 15; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
|||||
DB 1 GCTCTAGATGAACG 15

RESULT 3
AAZ08704
ID AAZ08704 standard; DNA; 25 BP.
XX
AC AAZ08704;
XX
XX 20-OCT-1999 (first entry)
XX
XX Human telomerase RNA template PCR primer R3C.
DE
XX
XX Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
KW telomeric repeat amplification protocol; detection; PCR primer; ss.
KW
XX Synthetic.
OS
OS Homo sapiens.
XX
XX WO9941406-A1.
XX
XX 19-AUG-1999.
XX
XX 16-FEB-1999; 99WO-US03302.
XX
XX 16-FEB-1998; 98US-0074793.
XX
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Abruzzo LV, Highsmith E, Stamberg J, Strovel JW;
XX
XX WPI; 1999-508655/42.
XX
XX Detecting telomerase activity in non-cellular body fluid using a
PT modified telomeric repeat amplification protocol
PT
XX Disclosure; Page 16; 32pp; English.
PS

XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 15 BP; 5 A; 3 C; 4 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 15; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
|||||
DB 1 GCTCTAGATGAACG 15

RESULT 2
AAV41176
ID AAV41176 standard; DNA; 19 BP.
XX
AC AAV41176;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 21ab.
DE
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW
XX immune system down-regulation; immuno-suppression; therapeutic; hTR;
KW
XX Synthetic.
OS
OS Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX
XX WPI; 1998-377670/32.
XX

XX A method has been developed for detecting telomerase activity in a
 CC non-cellular portion of body fluid from a cancer patient using a
 CC modified telomeric repeat amplification protocol (TRAP). A method for
 CC detecting cancer comprises: (a) removing the cellular portion of a body
 CC fluid specimen from the patient; (b) preparing a protein extract from
 CC the body fluid remainder; (c) assaying the extract for the presence and
 CC quantity of telomerase RNA or telomerase activity; and (d) comparing the
 CC results with normal levels, to determine the presence of cancer. The
 CC methods are used in cancer diagnosis and prognosis, and also to monitor
 CC cancer therapy effectiveness. Unlike prior art telomerase activity
 CC assays in cancer patients, the method allows noninvasive sample
 CC collection. The methods are also more reliable and less tumour specific
 CC than other methods which detect circulating tumour markers. The present
 CC sequence represents a human telomerase RNA template PCR primer used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTAACG 15
 DB 4 GCTCTAGAGTAACG 18

RESULT 4
 AAT10304
 ID AAT10304 standard; DNA; 26 BP.
 AC AAT10304;
 XX
 DT 10-SEP-1996 (first entry)
 XX
 DE RNA component of human telomerase nested PCR primer R3c.
 XX
 KW RNA component; human; telomerase; polymerase chain reaction;
 KW recombinant production; synthesis; mutant; detection; mammalian;
 KW identification; modulating agent; neoplastic condition;
 KW transcriptional regulatory sequence; gene therapy; disease;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601835-A1.
 XX
 PD 25-JAN-1996.

PF 06-JUL-1995; 95WO-US08530.
 XX
 PR 07-JUN-1995; 95US-0482115.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 07-JUN-1995; 95US-0472802.
 XX
 PA (GERO-) GERON CORP.

PI Andrews WH, Feng J, Funk W, Villeponteau B;
 XX
 DR WPI; 1996-097581/10.
 XX
 PT RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents
 XX
 PS Example 10; Page 82; 114pp; English.

XX The present sequence, a nested PCR primer for the RNA component
 CC of human telomerase (RCHT), was used in a 5' RACE procedure. The
 CC RCHT can be used in the recombinant prodn. of an active telomerase
 CC mol., capable of adding sequences to chromosomal DNA telomeres, and
 CC in the synthesis of mutant sequences for the detection of mutant

CC mammalian telomerase RNA component polynucleotides. The RCHT may
 CC also be used in the identification of telomerase modulating agents,
 CC and in the detection of telomerase related, or neoplastic
 CC conditions in a patient. Polynucleotides of at least 25
 CC consecutive nucleotides identical, or complementary to the RCHT
 CC sequence linked to heterologous transcriptional regulatory
 CC sequences, can be used for the gene therapy of human diseases.
 XX

SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTAACG 15
 DB 5 GCTCTAGAGTAACG 19

RESULT 5
 AAT10299
 ID AAT10299 standard; DNA; 26 BP.
 XX
 AC AAT10299;

XX
 DT 09-SEP-1996 (first entry)

XX RNA component of human telomerase antisense plasmid PCR primer R3C.
 DE
 XX RNA component; human; telomerase; lung fibroblast; cell line WI-38;
 KW recombinant production; synthesis; mutant; detection; mammalian;
 KW identification; modulating agent; neoplastic condition;
 KW transcriptional regulatory sequence; gene therapy; disease;
 KW polymerase chain reaction; antisense plasmid; PCR primer; ss.

XX Synthetic.

OS
 XX
 PN WO9601835-A1.

XX
 PD 25-JAN-1996.

XX
 PF 06-JUL-1995; 95WO-US08530.

XX
 PR 07-JUN-1995; 95US-0482115.

XX
 PR 07-JUL-1994; 94US-0272102.

XX
 PR 27-OCT-1994; 94US-0330123.

XX
 PR 07-JUN-1995; 95US-0472802.

XX
 PA (GERO-) GERON CORP.

XX
 PI Andrews WH, Feng J, Funk W, Villeponteau B;

XX
 DR WPI; 1996-097581/10.

XX
 PT RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents

XX
 PS Example 8; Page 80; 114pp; English.

XX The present sequence is a PCR primer for a RNA component of human
 CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
 CC genomic DNA library obtd. from the human lung fibroblast cell line
 CC WI-38. The RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene
 CC therapy of human diseases.

SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3; 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 6
AAT11044
ID AAT11044 standard; DNA; 26 BP.
XX
AC AAT11044;
XX
DT 02-JUL-1996 (first entry)
XX
DE Primer for production of telomerase antisense oligonucleotide.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
KW plasmid; probe; primer; ribozyme; ss.
XX
OS Synthetic.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US08620.
XX
PR 07-JUN-1995; 95US-0485778.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 13-FEB-1995; 95US-0387524.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
PA
XX Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
PI Marhuenda MA, Villeponteau B;
XX
XX WPI; 1996-097428/10.
XX
XX RNA components of (non)human mammalian telomerase(s) - useful in
PT studying cell senescence and immortalisation
PT
XX
XX Example 8; Page 53; 85pp; English.
XX
XX The RNA components of (non) human mammalian telomerase(s) especially
CC from mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the
CC telomerase; probes and primers can be used in detection; vectors and
CC host cells transformed with the isolated telomerase genes can be
CC used for production of telomerases; RNA and DNA ribozymes and triplex
CC forming oligonucleotides directed against the telomerase genes can
CC be used therapeutically as can plasmids. A mouse which lacks the
CC telomerase gene (also claimed) can be used for study of telomere
CC regulation in vivo, and the role it plays in immortalisation.
CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
CC antisense oligonucleotides which were then used to produce antisense
CC expression plasmids. AAT11040 was used alongside both AAT11043 and
CC AAT11044 to produce two different antisense molecules.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3; 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

Db 5 GCTCTAGATGAACG 19

RESULT 7
AAT58811
ID AAT58811 standard; DNA; 26 BP.
XX
AC AAT58811;
XX
DT 20-NOV-1997 (first entry)
XX
DE Human telomerase PCR 3'-primer R3C.
XX
KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
KW protozoa; tumour; antibody; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9640868-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09517.
XX
PR 07-JUN-1995; 95US-0478352.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA Autexier C, Greider C;
XX
XX WPI; 1997-099928/09.
XX
XX DNA encoding essential RNA components of human telomerase - also
PT truncated or recombinant telomerase, useful for diagnosis and
PT treatment of cancer and infection by eukaryotic parasites
XX
XX Example 5; Page 32; 48pp; English.
XX
XX The present sequence represents PCR 3'-primer R3C used for
CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
CC hybridisation assays to detect or quantify telomerase activity in cells,
CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
CC (yeast and protozoa) or tumours. It is also useful as primers for
CC amplification assays. The truncated or recombinant vertebrate telomerase
CC is used therapeutically to increase telomerase activity (also as
CC reagents in the screening assay) while the RNA or other inhibitors such
CC as antisense molecules, are used to reduce such activity. Typical
CC applications are initiation/restoration of activity to cause senescence
CC or to prevent immortalisation of cells in tumours or parasites. The DNA
CC is also used to produce recombinant telomerase, which can then be used
CC conventionally to raise antibodies for diagnostic detection of
CC telomerase. Detecting telomerase allows early diagnosis of tumour or
CC infection, before clinical signs manifest. Telomerase inhibitors
CC directed against e.g. Trypanosoma should cause fewer side effects than
CC drugs currently used to treat such infections. The DNA encodes those
CC parts of hTR RNA essential for activity but are significantly shorter
CC than the endogenous RNA component.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 8
AAV19489
ID AAV19489 standard; DNA; 26 BP.

```

XX AAV19489;
AC
XX
XX 28-AUG-1998 (first entry)
XX
XX Human hTR gene RT-PCR primer R3c.
DE
XX
XX hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;
KW Gene therapy; diagnosis; PCR; primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9811204-A1.
FN
XX
XX 19-MAR-1998.
XX
XX 13-SEP-1996; 96WO-US14679.
XX
XX 13-SEP-1996; 96WO-US14679.
XX (GERO-) GERON CORP.
XX
XX Adams RR, Andrews WH, Feng J, Villeponteau B;
PI
XX
XX WPI; 1998-207373/18.
DR
XX
XX Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT telomerase activity
PT
XX
XX Disclosure; Page 49; 86pp; English.
XX
XX Primers R3c and F3b (see AAV19488) were designed for the PCR
CC amplification of the human telomerase hTR gene (see AAV19481). hTR
CC mRNA levels were showed to correlate with telomerase activity
CC levels in a variety of mortal and immortal cell lines. Methods of
CC the invention allow detection and quantitation of TPC2 (see
CC AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be
CC used to detect immortal cells, especially telomerase positive
CC cancer cells.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 15; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 9
AAV17033
ID AAV17033 standard; DNA; 26 BP.
XX
XX AAV17033;
AC
XX
XX 13-AUG-1998 (first entry)
DE
XX
XX Telomerase PCR primer R3c.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
KW PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX GB2317891-A.
PN
XX
XX 08-APR-1998.
PD
XX
XX

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PF 01-OCT-1997; 97GB-0020890.
XX
XX 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
PA
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
PI Morin GB, Nakamura T, Harley CB;
XX
XX WPI; 1998-171633/16.
DR
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of
PT cell proliferation conditions especially cancer and ageing
XX
XX Example 2; Page 218; 387pp; English.
XX
XX The present sequence represents a PCR primer from the present invention
CC which describes human telomerase reverse transcriptase (hTERT). The
CC present invention also describes the following methods: (A) determining
CC whether a test compound is a modulator of hTERT, by detecting the change
CC in hTERT recombinant protein or polynucleotide, on administration of the
CC compound; (B) preparation of recombinant telomerase by contacting a
CC protein preparation of hTERT with a telomerase RNA component; (C)
CC detection of the hTERT RNA or protein in a sample by binding a relevant
CC probe to the sample and detecting the complex formed or in the case of
CC RNA detection, amplifying the product and correlating the presence of
CC complex or amplification product with presence of hTERT in the sample;
CC and (D) increasing the proliferation of a vertebrate cell by increasing
CC hTERT expression; and (E) the use of an agent that causes an increase in
CC cell vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be
CC used to treat conditions that are associated with high telomerase
CC activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 15; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 10
AAV90788
ID AAX90788 standard; DNA; 26 BP.
XX
XX AAX90788;
AC
XX
XX 13-JAN-2000 (first entry)
DE
XX
XX Human telomerase RNA specific PCR primer-2.
XX
XX PCR primer; human telomerase RNA; hTR; amplify; human staufer cDNA;
KW htau; synthesised; random hexamer primer;
KW Superscript II reverse transcriptase; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.

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XX WO9951255-A1.
 XX
 XX PD 14-OCT-1999.
 XX
 XX PF 06-APR-1999; 99WO-US07533.
 XX
 XX PR 06-APR-1998; 98US-0080783.
 XX
 XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX PI Greider CW, Le S;
 XX
 XX WI 1999-620168/53.
 XX
 XX PT Human stauften polypeptide useful in methods for identifying telomerase
 XX inhibitors -
 XX
 XX PS Disclosure; Page 15; 50pp; English.
 XX
 XX CC The present sequence is a PCR primer specific to human telomerase
 XX RNA (hTR). It is used to amplify human stauften (hStau) cDNA synthesised
 XX CC using random hexamer primers and Superscript II reverse transcriptase.
 XX
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 DB 5 GCTCTAGAATGAACG 19
 RESULT 11
 AAX77402
 ID AAX77402 standard; DNA; 26 BP.
 XX
 XX AC AAX77402;
 XX
 XX DT 05-AUG-1999 (first entry)
 XX
 XX DE Human telomerase RNA PCR primer TE-hTR3.1.
 XX
 XX KW Telomerase; human; diagnosis; bladder cancer; detection; urine;
 XX KW PCR primer; ss.
 XX
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX
 XX PN EP926245-A2.
 XX
 XX PD 30-JUN-1999.
 XX
 XX PF 21-DEC-1998; 98EP-0124326.
 XX
 XX PR 22-DEC-1997; 97DE-1057300.
 XX
 XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 XX PI Emrich T;
 XX
 XX WI 1999-349242/30.
 XX
 XX PT Detecting telomerase RNA in urine - useful for diagnosis of bladder
 XX cancer
 XX
 XX PS Claim 6; Page 10; 13pp; German.
 XX
 XX CC This invention describes a novel method for diagnosing bladder cancer,
 XX CC which comprises detecting telomerase RNA in a urine sample. The method
 XX CC of the invention has greater sensitivity and reliability than assays for

CC telomerase activity (cf. WO 9735871). This sequence represents a primer
 CC used in the method of the invention.
 XX
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 DB 5 GCTCTAGAATGAACG 19
 RESULT 12
 AAX01542
 ID AAX01542 standard; DNA; 26 BP.
 XX
 XX AC AAX01542;
 XX
 XX DT 29-APR-1999 (first entry)
 XX
 XX DE PCR primer for Human TPC3 gene.
 XX
 XX KW TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;
 XX KW fertility; diagnosis; therapy; PCR primer; ss.
 XX
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX
 XX PN US5858777-A.
 XX
 XX PD 12-JAN-1999.
 XX
 XX PF 13-SEP-1996; 96US-0710249.
 XX
 XX PR 08-SEP-1995; 95US-0003492.
 XX
 XX PR 05-JAN-1996; 96US-0583808.
 XX
 XX PR 13-SEP-1996; 96US-0710249.
 XX
 XX PA (GERO-) GERON CORP.
 XX
 XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
 XX
 XX WI 1999-152104/13.
 XX
 XX KW DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere
 XX length or modulating telomerase activity
 XX
 XX PS Example; Column 38; 59pp; English.
 XX
 XX CC This sequence represents a PCR primer for DNA encoding the human TPC3
 XX protein, which is contained within the recombinant mammalian host cell of
 XX the invention. The invention provides methods and reagents for regulating
 XX telomere length and modulating telomerase activity in mammalian cells as
 XX well as for detecting, diagnosing, and treating related diseases and
 XX conditions such as cancer, pregnancy, or fertility in humans and other
 XX mammals.
 XX
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 DB 5 GCTCTAGAATGAACG 19
 RESULT 13
 AAA88250
 ID AAA88250 standard; DNA; 26 BP.

XX AAA88250;
 AC 15-DEC-2000 (first entry)
 DT Human telomerase RNA reverse transcriptase PCR primer #2.
 DE Human; telomerase; hTR; reverse transcriptase; RT-PCR; PCR primer;
 DE detection; cancer; micrometastasis; diagnosis; ss.
 KW Homo sapiens.
 OS WO200046601-A1.
 PN 10-AUG-2000.
 PD 01-FEB-2000; 2000WO-1B00100.
 XX 02-FEB-1999; 99GB-0002302.
 PF (LARS/) LARSEN F.
 PR (SKAA/) SKAANSENG M.
 XX Larsen F, Skaanseng M;
 PI WPI; 2000-491281/43.
 DR Detecting telomerase activity in samples, useful for diagnosis of
 XX cancer and micrometastasis, comprises treating sample with solid phase,
 PT removing solid phase and treating to elute bound telomerase -
 PT Example 11; Page 38; 69pp; English.
 PS The present invention describes a method (I) for detecting telomerase
 XX activity in a sample. The method comprises treating the sample with a
 CC solid phase to bind telomerase, separating the solid phase from the
 CC sample to form a test sample which may be treated to elute bound
 CC telomerase and assaying the sample for telomerase activity. Also
 CC described are: (1) a kit (II) for detecting telomerase activity,
 CC comprising a solid phase and one or more components for assaying
 CC telomerase activity; and (2) a component (III) of an assay system for
 CC detecting telomerase activity, comprising a solid phase for binding
 CC telomerase on which is present a substrate for telomerase elongation.
 CC (I) is useful for cancer diagnosis or prognosis and detection of
 CC micrometastasis as detection of telomerase activity is indicative of
 CC cancer or micrometastasis. The solid phase used in (I) is useful for
 CC separating telomerase from a sample and therefore for detecting
 CC telomerase activity. (II) is useful for detection of cancer cells and
 CC may also comprises means for assaying an mRNA diagnostic for cancer.
 CC The present sequence represents a reverse transcriptase (RT) PCR primer
 CC for human telomerase RNA, which is used in an example from the present
 CC invention.
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 15; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGATGAACG 15
 Db 5 GCTCTAGATGAACG 19
 RESULT 14
 ABK48024
 ID ABK48024 standard; DNA; 26 BP.
 XX
 AC ABK48024;
 XX
 DT 18-JUN-2002 (first entry)
 DE Human telomerase-associated RNA template (hTR), PCR primer hTR2.

XX Human; telomerase-associated RNA template; hTR; endometrial;
 KW malignancy; cancer; breast; ovarian; head and neck; lung; cervical;
 KW colorectal; gastric; liver; pancreatic; bladder; prostate;
 KW brain; kidney; oesophagus; melanoma; sarcoma; premalignancy;
 KW carcinoma in-situ; cervical dysplasia; bronchial dysplasia;
 KW cervical intraepithelial neoplasia; atypical hyperplasia;
 KW colorectal adenoma; atypical endometrial hyperplasia; tumour;
 KW Barrett's oesophagus; telomerase-directed therapy; primer; ss.
 XX Homo sapiens.
 OS WO200218652-A2.
 PN 07-MAR-2002.
 PD 28-AUG-2001; 2001WO-US26749.
 XX 31-AUG-2000; 2000US-0653573.
 PR (ONCO-) ONCOMEDX INC.
 PA Kopreski MS, Gocke CD;
 XX WPI; 2002-269532/31.
 DR Detecting human telomerase RNA template RNA or human telomerase reverse
 XX transcriptase protein RNA in bodily fluid, useful as marker for
 PT diagnosing, monitoring or treating cancer, carcinoma in situ or
 PT premalignancy -
 XX Example 1; Page 14; 30pp; English.
 PS The invention relates to detecting human telomerase RNA template (hTR)
 CC RNA or human telomerase reverse transcriptase protein RNA (hRTP) RNA (I)
 CC in a bodily fluid, comprising amplifying RNA extracted from plasma or
 CC serum sample, or its corresponding cDNA comprising (I), using primers or
 CC probes that target (I) or cDNA and detecting qualitatively or
 CC quantitatively amplified product of (I) or cDNA product. The method is
 CC useful for detecting (I) in a bodily fluid, which is useful for
 CC identifying a human having (I) expressing cells or tissue which
 CC include a malignancy preferably a cancer of breast, ovarian, head and
 CC neck, lung, cervical, colorectal, gastric, liver, pancreatic, bladder,
 CC prostate, endometrial, brain, kidney, or oesophagus, or a melanoma or
 CC sarcoma, premalignancy or carcinoma in-situ, preferably cervical
 CC dysplasia, cervical intraepithelial neoplasia, bronchial dysplasia,
 CC atypical hyperplasia of the breast, ductal carcinoma in-situ,
 CC colorectal adenoma, atypical endometrial hyperplasia, or Barrett's
 CC oesophagus, where the human is at risk for developing a malignancy or
 CC premalignancy or is known to have malignancy, premalignancy or
 CC carcinoma in situ. The method is also useful for treating a human with
 CC cancer for the telomerase-directed therapy, which comprises selecting the
 CC cancer for the therapy after detection of (I), for determining a
 CC need for diagnostic test in a human with malignancy or premalignancy
 CC and for monitoring a therapy administered to a human. (I) provides a
 CC marker which is utilised as a guide to whether adequate therapeutic
 CC effect has been achieved, or whether additional or more advanced therapy
 CC is required, and to assess prognosis in these patients. The method also
 CC allows identification or analysis, either quantitatively or
 CC qualitatively, of (I) in plasma or serum of humans during or following
 CC surgical procedures to remove premalignant or malignant lesions, and thus
 CC allow stratification of such patients as to their risk of residual
 CC cancer following surgery, and their need for further therapy or who has
 CC completed therapy as an early indicator or relapsed cancer, impending
 CC relapse, or treatment failure. The method allows the development and
 CC application of telomerase-specific therapy even when only premalignant
 CC tumours, early cancer, or occult cancer or metastasis such as following
 CC resection or in minimal residual disease are present. The present
 CC sequence represents a PCR primer for human telomerase-associated
 CC RNA template (hTR).
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ

Query Match 100.0%; Score 15; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 15

AAD24246
ID AAD24246 standard; DNA; 26 BP.
XX
AC AAD24246;
XX
DT 07-MAR-2002 (first entry)
XX
DE Human telomerase (hTR) cDNA amplifying R3c downstream RT-PCR primer.
XX
KW Human; telomerase; TR; telomerase activity-related disease; therapy;
KW cancer; pregnancy; fertility; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
FN US6300110-B1.
XX
PD 09-OCT-2001.
XX
PF 23-DEC-1998; 98US-0220157.
XX
PR 09-SEP-1995; 95US-003492P.
PR 13-SEP-1996; 96US-0710249.
PR 05-JAN-1996; 96US-0583808.
XX
PA (GERO-) GERON CORP.
XX
PI Villeponteau B, Peng J, Andrews WH, Adams RR;
XX
DR WPI; 2002-033174/04.
XX
PT Peptide products of the human TPC2 and TPC3 gene are involved in
PT regulation of telomere length and activity are useful to diagnose and
PT treat telomere length and activity-related diseases -
XX
PS Example; Column 38; 60pp; English.
XX
CC The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is a reverse transcription (RT) PCR primer
CC used for amplifying human telomerase (hTR) cDNA.
XX
SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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SUMMARIES

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4	15	100.0	26	6	AR016055	AR016055 Sequence
5	15	100.0	26	6	AR028786	AR028786 Sequence
6	15	100.0	26	6	AR059216	AR059216 Sequence
7	15	100.0	26	6	AR075527	AR075527 Sequence
8	15	100.0	26	6	AR161925	AR161925 Sequence
9	15	100.0	26	6	AX022187	AX022187 Sequence
10	15	100.0	26	6	AX033377	AX033377 Sequence
11	15	100.0	26	6	AX468455	AX468455 Sequence
12	15	100.0	26	6	BD011297	BD011297 Human tel
13	15	100.0	26	6	E36508	E36508 Method for
14	15	100.0	26	6	E37046	E37046 Human telom
15	15	100.0	26	6	I31770	I31770 Sequence 23
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18	15	100.0	30	6	AR063832	AR063832 Sequence
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28	12	80.0	26	6	AR169136	AR169136 Sequence
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30	12	80.0	26	6	AX036237	AX036237 Sequence
31	12	80.0	30	6	I25474	I25474 Sequence 3
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34	12	80.0	39	6	E50834	E50834 Novel G pro
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37	11	73.3	21	6	AR193717	AR193717 Sequence
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40	11	73.3	22	6	AX370655	AX370655 Sequence
41	11	73.3	23	6	AR112025	AR112025 Sequence
42	11	73.3	24	6	A91468	A91468 Sequence 10
43	11	73.3	24	6	AX085592	AX085592 Sequence
44	11	73.3	26	6	AR179447	AR179447 Sequence
45	11	73.3	27	6	AX175102	AX175102 Sequence

ALIGNMENTS

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DEFINITION Sequence 10 from patent US 5846723.
ACCESSION AR063834
VERSION AR063834.1 GI:5993142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, N. Woo., Wu, F., Kealey, J. T., Pruzan, R. and Weinrich, S. L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 10 08-DEC-1998;
FEATURES Location/Qualifiers

AR063834 15 bp DNA linear PAT 29-SEP-1999

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LOCUS AR063833 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5846723.
ACCESSION AR063833
VERSION AR063833.1 GI:5993141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 9 08-DEC-1998;
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DEFINITION Sequence 2 from Patent EP0926245.
ACCESSION A94988
VERSION A94988.1 GI:6779168
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Emrich,T.D.
TITLE Method for detection of carcinoma of the urinary bladder within a
JOURNAL urine sample
PATENT: EP 0926245-A 2 30-JUN-1999;
JOURNAL ROCHE DIAGNOSTICS GMBH (DE)
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DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES
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DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methods and reagents for regulating telomere length and telomerase
JOURNAL activity
PATENT: US 5858777-A 26 12-JAN-1999;
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DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
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TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
FEATURES Location/Qualifiers
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DEFINITION Sequence 24 from patent US 5958680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
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LOCUS AR161925 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
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Db 5 GCTCTAGATGAACG 19

RESULT 9
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DEFINITION Sequence 26 from Patent EP0953042.
ACCESSION AX022187
VERSION AX022187.1 GI:10045855
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Andrews,W.H., Villeponteau,B., Adams,R.R. and Feng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 26 03-NOV-1999;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t
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DEFINITION Sequence 9 from Patent WO0046601.
ACCESSION AX033377
VERSION AX033377.1 GI:10280151
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 9 10-AUG-2000;
FEATURES Location/Qualifiers
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ORIGIN

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
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LOCUS AX468455 26 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION AX468455
VERSION AX468455.1 GI:21901291
KEYWORDS

SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Kopreski, M.S. and Gocke, C.D.
 TITLE Method for detection of htr and htert telomerase-associated rna in
 JOURNAL plasma or serum
 Patent: WO 0218652-A 5 07-MAR-2002;
 Oncomedx, Inc. (US)
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 LOCUS BD011297 26 bp DNA linear PAT 31-JAN-2002
 DEFINITION Human telomerase catalytic subunit.
 ACCESSION BD011297
 VERSION BD011297.1 GI:18639670
 KEYWORDS JP 2001081042-A/254.
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,
 Harley, C.B. and Andrews, W.H.
 TITLE Human telomerase catalytic subunit
 JOURNAL Human telomerase catalytic subunit
 Patent: JP 2001081042-A 254 27-MAR-2001;
 JERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 2001081042-A/254
 PD 27-MAR-2001
 PF 27-JUL-2000 JP 2000227474
 PR 01-OCT-1996 US 08/724663, 18-APR-1997 US 08/844419 PR
 25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR
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 R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
 MORIN,
 PI CALVIN B HARLEY, WILLIAM H ANDREWS
 PC A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
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 DEFINITION Method for detecting bladder cancer in urine samples.
 ACCESSION E36508
 VERSION E36508.1 GI:13022705
 KEYWORDS JP 1999243995-A/2.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Thomas, E.
 TITLE Method for detecting bladder cancer in urine samples
 JOURNAL Patent: JP 1999243995-A 2 14-SEP-1999;
 ROCHE DIAGNOSTICS GMBH
 COMMENT OS Artificial Sequence
 PN JP 1999243995-A/2
 PD 14-SEP-1999
 PF 22-DEC-1998 JP 1998365689
 PR 22-DEC-1997 DE 19757300.2
 PI THOMAS ENRIHI
 PC C12Q1/68//C12N1/00
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 LOCUS E37046 26 bp DNA linear PAT 18-JUN-2001
 DEFINITION Human telomerase catalytic subunit promoter.
 ACCESSION E37046
 VERSION E37046.1 GI:13023009
 KEYWORDS JP 1999253177-A/254.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
 Calvin, B.H. and William, H.A.
 TITLE Human telomerase catalytic subunit promoter
 JOURNAL Patent: JP 1999253177-A 254 21-SEP-1999;
 JERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 1999253177-A/254
 PD 21-SEP-1999
 PF 15-OCT-1998 JP 1998320169
 PR 01-OCT-1996 US 08/724.643, 18-APR-1997 US 08/844.419, PR
 25-APR-1997 US 08/846.017, 06-MAY-1997 US 08/851.843, PR
 09-MAY-1997 US 08/854.050, 14-AUG-1997 US 08/911.312, PR

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Sequence: 1

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11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	18	6	US-09-721-456-543
2	11	100.0	18	9	US-10-325-810-543
3	11	100.0	21	1	PCT-US03-05708-27
4	11	100.0	21	1	PCT-US03-05708-202
5	11	100.0	21	1	PCT-US03-04088-539
6	11	100.0	21	1	PCT-US03-04088-543
7	11	100.0	21	1	PCT-US03-04088-547
8	11	100.0	21	1	PCT-US03-04088-551
9	11	100.0	21	1	PCT-US03-04088-555
10	11	100.0	21	1	PCT-US03-04088-559
11	11	100.0	21	10	US-10-374-366-27
12	11	100.0	21	10	US-10-374-366-202
13	11	100.0	22	9	US-10-188-523B-5
14	11	100.0	22	9	US-10-188-523C-5
15	11	100.0	23	1	PCT-US03-04088-520
16	11	100.0	23	1	PCT-US03-04088-521
17	11	100.0	23	9	US-10-310-188-36216
18	11	100.0	24	5	US-09-807-809A-5
19	11	100.0	25	7	US-09-954-445A-66031
20	11	100.0	25	9	US-10-355-577-393144

21	11	100.0	25	9	US-10-355-577-396066
22	11	100.0	25	9	US-10-355-577-924166
c 23	11	100.0	25	12	US-60-427-808-6866
24	11	100.0	25	12	US-60-427-808-62369
25	11	100.0	25	12	US-60-427-808-104137
c 26	11	100.0	25	12	US-60-427-808-115885
27	11	100.0	25	12	US-60-427-808-137579
c 28	11	100.0	25	12	US-60-427-808-301228
29	11	100.0	25	12	US-60-427-808-397410
30	11	100.0	25	12	US-60-427-808-420914
c 31	11	100.0	25	12	US-60-427-808-425838
32	11	100.0	25	12	US-60-427-808-469846
c 33	11	100.0	25	12	US-60-427-808-666732
34	11	100.0	25	12	US-60-427-808-681847
35	11	100.0	25	12	US-60-427-808-681848
36	11	100.0	25	12	US-60-427-808-887509
37	11	100.0	25	12	US-60-427-808-952738
38	11	100.0	25	12	US-60-427-836-248462
39	11	100.0	25	12	US-60-427-836-248463
c 40	11	100.0	25	12	US-60-427-836-280388
c 41	11	100.0	25	12	US-60-427-836-506901
c 42	11	100.0	25	12	US-60-427-836-612340
c 43	11	100.0	25	12	US-60-427-836-612342
44	11	100.0	26	1	PCT-US02-11134-11
45	11	100.0	26	1	PCT-US02-11134-13

ALIGNMENTS

RESULT 1

US-09-721-456-543

; Sequence 543, Application US/09721456

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-Nov-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

APPLICATION NUMBER: US 08/911,312

;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 35,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 543:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "antisense hTERT molecule"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-456-543

Query Match 100.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 2
US-10-325-810-543
; Sequence 543, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ausubus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 543:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "antisense hTERT molecule"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-10-325-810-543

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 3
PCT-US03-05708-27
; Sequence 27, Application PC/TUS0305708
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/05708
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer 18-5'
PCT-US03-05708-27

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

```
Db          3  GCTCTAGAATG 13

RESULT 4
PCT-US03-05708-202
; Sequence 202, Application PC/TUS0305708
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/05708
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202
; TYPE: DNA
; ORGANISM: Rhodospiridium glutinis
PCT-US03-05708-202

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGAATG 11
      |||||
Db      3  GCTCTAGAATG 13

RESULT 5
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGAATG 11
      |||||
Db      3  GCTCTAGAATG 13

RESULT 6
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-543

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGAATG 11
      |||||
Db      19 GCTCTAGAATG 9

RESULT 7
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
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;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/396,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 547
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: sRNA sense region
;; NAME/KEY: misc feature
;; LOCATION: (1)..(2)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
;; NAME/KEY: misc feature
;; LOCATION: (4)..(5)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (7)..(9)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (11)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (19)..(19)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; NAME/KEY: misc feature
;; LOCATION: (21)..(21)
;; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATG 11
|||||
Db 19 GCTCTAGAAATG 9

RESULT 8
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid

;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 551
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
;; OTHER INFORMATION: antisense region
;; NAME/KEY: misc feature
;; LOCATION: (2)..(5)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (10)..(10)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (14)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (17)..(17)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; NAME/KEY: misc feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; NAME/KEY: misc feature
;; LOCATION: (20)..(20)
;; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-551

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred.No. 5.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATG 11
|||||
Db 1 GCUCUAGAAUG 11

RESULT 9
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

```
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555
Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
Db 19 GCTCTAGATG 9
RESULT 10
PCT-US03-04088-559
; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(9)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

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Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTAGAATG 11
||:||||:|
Db 1 GCUCUAGAUG 11

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RESULT 11
US-10-374-366-27
; Sequence 27, Application US/10374366
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 US NA
; CURRENT APPLICATION NUMBER: US/10/374,366
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer 18-5'
US-10-374-366-27

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```

Query Match 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GCTCTAGAATG 11
|||||||
Db 3 GCTCTAGAATG 13

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RESULT 12
US-10-374-366-202
; Sequence 202, Application US/10374366
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 US NA

```

```

; CURRENT APPLICATION NUMBER: US/10/374,366
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Rhodospiridium glutinis
US-10-374-366-202

```

```

Query Match 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GCTCTAGAATG 11
|||||||
Db 3 GCTCTAGAATG 13

```

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RESULT 13
US-10-188-523B-5
; Sequence 5, Application US/10188523B
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US DIVCIP
; CURRENT APPLICATION NUMBER: US/10/188,523B
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-188-523B-5

```

```

Query Match 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GCTCTAGAATG 11
|||||||
Db 3 GCTCTAGAATG 13

```

```

RESULT 14
US-10-188-523C-5
; Sequence 5, Application US/10188523C
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009-CIP
; CURRENT APPLICATION NUMBER: US/10/188,523C
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: MICROSOFT OFFICE 97
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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;; OTHER INFORMATION: primer
US-10-188-523C-5

Query Match 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11
|||
DB 3 GCTCTAGAATG 13

RESULT 15
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 100.0%; Score 11; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11
|||
DB 23 GCTCTAGAATG 13

Search completed: June 26, 2003, 04:15:20
Job time : 264.081 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 453.88 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGACGGTGG 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New.*

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- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
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- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	21	1	PCT-US03-04088-539
C 2	19	100.0	21	1	PCT-US03-04088-539
C 3	19	100.0	21	1	PCT-US03-04088-547
C 4	19	100.0	21	1	PCT-US03-04088-551
C 5	19	100.0	21	1	PCT-US03-04088-555
C 6	19	100.0	21	1	PCT-US03-04088-559
C 7	19	100.0	23	1	PCT-US03-04088-520
C 8	19	100.0	23	1	PCT-US03-04088-521
9	19	100.0	26	6	US-09-721-456-598
10	19	100.0	26	9	US-10-325-810-598
11	19	100.0	26	9	US-10-359-935-23
12	19	100.0	30	10	US-10-330-872-5
13	19	100.0	30	10	US-10-330-872A-5
C 14	17	89.5	21	1	PCT-US03-04088-538
C 15	17	89.5	21	1	PCT-US03-04088-542
C 16	17	89.5	21	1	PCT-US03-04088-546
C 17	17	89.5	21	1	PCT-US03-04088-550
C 18	17	89.5	21	1	PCT-US03-04088-554
C 19	17	89.5	21	1	PCT-US03-04088-558
20	16.4	86.3	18	6	US-09-721-456-543

21	16.4	86.3	18	9	US-10-325-810-543	Sequence 543, App
22	14.8	77.9	25	9	US-10-355-577-751232	Sequence 751232, A
C 23	14.4	75.8	25	9	US-10-355-577-70333	Sequence 70333, A
24	14.2	74.7	25	7	US-09-954-445A-54976	Sequence 54976, A
C 25	14	73.7	23	9	US-10-310-188-36216	Sequence 36216, A
26	14	73.7	23	8	US-10-442-506-39	Sequence 39, Appl
27	14	73.7	25	12	US-60-427-808-952738	Sequence 952738, A
28	14	73.7	25	13	US-60-469-545-13722	Sequence 13722, A
C 29	14	73.7	25	13	US-60-469-545-222991	Sequence 222991, A
C 30	13.8	72.6	25	9	US-10-098-263B-64498	Sequence 64498, A
31	13.8	72.6	25	9	US-10-355-577-44115	Sequence 44115, A
C 32	13.8	72.6	25	9	US-10-355-577-45101	Sequence 45101, A
C 33	13.8	72.6	25	9	US-10-355-577-134105	Sequence 134105, A
C 34	13.8	72.6	25	12	US-60-427-808-304013	Sequence 304013, A
C 35	13.8	72.6	25	12	US-60-427-808-666732	Sequence 666732, A
C 36	13.8	72.6	25	12	US-60-427-808-738286	Sequence 738286, A
C 37	13.8	72.6	25	12	US-60-427-836-279457	Sequence 279457, A
C 38	13.4	70.5	25	9	US-10-355-577-173196	Sequence 173196, A
C 39	13.4	70.5	25	9	US-10-355-577-544182	Sequence 544182, A
C 40	13.4	70.5	25	9	US-10-355-577-981444	Sequence 981444, A
41	13.4	70.5	25	12	US-60-417-190-74827	Sequence 74827, A
42	13.4	70.5	25	12	US-60-417-190-74828	Sequence 74828, A
43	13.4	70.5	25	12	US-60-417-190-74829	Sequence 74829, A
44	13.4	70.5	25	12	US-60-417-190-74830	Sequence 74830, A
45	13.4	70.5	25	12	US-60-417-190-74831	Sequence 74831, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04089
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626.
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 19; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 19 GCTCTAGATGAACGGTGG 1

RESULT 2

PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-543

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.2;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 1 GCUCUAGAUGAAGCGUGG 19

RESULT 3

PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 547
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxybasic moiety
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 19 GCTCTAGATGAACGGTGG 1

RESULT 4

PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

;; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 551
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
;; OTHER INFORMATION: antisense region
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2)..(5)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (10)..(10)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (14)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (17)..(17)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(20)
;; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-551

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.2;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGACGGTGG 19
||:|||||:|||||:
Db 1 GCUCUAGAAUGAACGGG 19

RESULT 5

PCT-US03-04088-555/c
;; Sequence 555, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwigen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 555
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
;; OTHER INFORMATION: region
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(2)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (3)..(3)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (4)..(5)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (6)..(6)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (7)..(9)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (10)..(10)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (11)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (15)..(18)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (19)..(19)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; FEATURE:

Query Match 100.0%; Score 19; DB 1; Length 23;

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 23 GCTCTAGAAATGAACGGTGG 5

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 100.0%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 21 GCTCTAGAAATGAACGGTGG 3

RESULT 9
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-09-721-456-598
SEQUENCE DESCRIPTION: SEQ ID NO: 598:

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 10
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
```

/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 23-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 23-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 598:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..26
/ OTHER INFORMATION: /note="R3c primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 11

US-10-359-935-23
/ Sequence 23, Application US/10359935
/ GENERAL INFORMATION:
/ APPLICANT: Villeponteau, Bryant
/ Feng, Junli
/ Funk, Walter
/ Andrews, William H.
/ TITLE OF INVENTION: Mammalian Telomerase
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/359,935
/ FILING DATE: 07-Feb-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/057,351
/ FILING DATE: 08-APR-1994
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 07-JUL-1994
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ APPLICATION NUMBER: US 08/472,802
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 015389-000821US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 12

US-10-330-872-5
/ Sequence 5, Application US/10330872
/ GENERAL INFORMATION:
/ APPLICANT: Geron Corporation
/ APPLICANT: Weinrich, Scott
/ APPLICANT: Atkinson III, Edward
/ APPLICANT: Lichtsteiner, Serge
/ APPLICANT: Vasserot, Alain
/ APPLICANT: Pruzan, Ronald
/ TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
/ TITLE OF INVENTION: Inhibitors
/ FILE REFERENCE: 011/006C

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; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAAATGAACGGTGG 19
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Db      1 GCCTAGAAATGAACGGTGG 19

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAAATGAACGGTGG 19
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Db      1 GCCTAGAAATGAACGGTGG 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James

```

```

; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-538

Query Match      89.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TCTAGAAATGAACGGTGG 19
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Db      19 TCTAGAAATGAACGGTGG 3

RESULT 15
PCT-US03-04088-542
; Sequence 542, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15

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; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-542

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Query Match      89.5%; Score 17; DB 1; Length 21;
Best Local Similarity 76.5%; Pred. No. 28;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 TCTAGATGAACGGTGG 19
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Db      1 UCUGAUAUGACGGUGG 17

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Search completed: June 26, 2003, 04:15:18
Job time : 454.188 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1612.2 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGACCGTGG 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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- 72: /cgn2_6/ptodata/2/pna/US6028 COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6029 COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6031 COMB.seq.*
- 76: /cgn2_6/ptodata/2/pna/US6032 COMB.seq.*
- 77: /cgn2_6/ptodata/2/pna/US6033 COMB.seq.*
- 78: /cgn2_6/ptodata/2/pna/US6034 COMB.seq.*
- 79: /cgn2_6/ptodata/2/pna/US6035 COMB.seq.*
- 80: /cgn2_6/ptodata/2/pna/US6036 COMB.seq.*
- 81: /cgn2_6/ptodata/2/pna/US6037 COMB.seq.*
- 82: /cgn2_6/ptodata/2/pna/US6038 COMB.seq.*
- 83: /cgn2_6/ptodata/2/pna/US6039 COMB.seq.*
- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	PCT-US97-23619-9 Sequence 9, Appli
2	19	100.0	19	11	US-08-770-564A-9 Sequence 9, Appli
3	19	100.0	25	16	US-09-250-336A-4 Sequence 4, Appli
4	19	100.0	25	25	US-09-642-177-4 Sequence 4, Appli
5	19	100.0	26	1	PCT-US96-14679-27 Sequence 27, Appli
6	19	100.0	26	1	PCT-US96-14679A-27 Sequence 27, Appli
7	19	100.0	26	1	PCT-US99-03302-4 Sequence 4, Appli
8	19	100.0	26	1	PCT-US99-07533-4 Sequence 4, Appli
9	19	100.0	26	1	PCT-US99-07533-4 Sequence 4, Appli
10	19	100.0	26	6	US-08-272-102-23 Sequence 23, Appli
11	19	100.0	26	7	US-08-387-524-19 Sequence 19, Appli
12	19	100.0	26	8	US-08-472-802A-24 Sequence 24, Appli
13	19	100.0	26	8	US-08-472-802B-24 Sequence 24, Appli
14	19	100.0	26	8	US-08-482-115A-23 Sequence 23, Appli
15	19	100.0	26	9	US-08-520-550-19 Sequence 19, Appli
16	19	100.0	26	9	US-08-521-634-41 Sequence 41, Appli
17	19	100.0	26	10	US-08-660-678-23 Sequence 23, Appli
18	19	100.0	26	13	US-08-911-312-23 Sequence 23, Appli
19	19	100.0	26	13	US-08-911-312A-23 Sequence 23, Appli
20	19	100.0	26	13	US-08-912-951-312 Sequence 312, App
21	19	100.0	26	13	US-08-973-589-17 Sequence 17, Appli

22 19 100.0 26 13 US-08-974-549-598
23 19 100.0 26 14 US-09-057-351-23
24 19 100.0 26 16 US-09-216-847-2
25 19 100.0 26 16 US-09-250-336-4
26 19 100.0 26 16 US-09-259-943-45
27 19 100.0 26 18 US-09-402-181A-598
28 19 100.0 26 18 US-09-402-181B-598
29 19 100.0 26 18 US-09-432-503-598
30 19 100.0 26 25 US-09-653-573-5
31 19 100.0 26 29 US-09-721-477-598
32 19 100.0 26 29 US-09-721-506-598
33 19 100.0 26 33 US-09-890-567-9
34 19 100.0 26 33 US-09-895-606-26
35 19 100.0 26 38 US-10-044-539-312
36 19 100.0 26 38 US-10-044-692-312
37 19 100.0 27 1 PCT-US97-23619-26
38 19 100.0 30 1 PCT-US97-23619-8
39 19 100.0 30 9 US-08-510-736-5
40 19 100.0 30 11 US-08-770-564A-8
41 19 100.0 30 21 US-09-540-119B-10
42 19 100.0 30 28 US-09-717-828A-5
43 19 100.0 30 28 US-09-717-828B-5
44 19 100.0 30 28 US-09-717-829A-5
45 19 100.0 30 34 US-09-903-461-2

ALIGNMENTS

RESULT 1
PCT-US97-23619-9
; Sequence 9, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

Sequence 598, App
Sequence 23, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 45, Appl
Sequence 598, App
Sequence 598, App
Sequence 5, Appl
Sequence 598, App
Sequence 9, Appl
Sequence 26, Appl
Sequence 312, App
Sequence 312, App
Sequence 26, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 2, Appl

; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..19
; OTHER INFORMATION: /note= "oligo 2lab"
PCT-US97-23619-9

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 1 GCTCTAGAAATGAACGGTGG 19

RESULT 2

US-08-770-564A-9
; Sequence 9, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-9

Query Match 100.0%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 1 GCTCTAGAAATGAACGGTGG 19

RESULT 3
US-09-250-336A-4

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; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: TELOMERASE ASSAY OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 100.0%; Score 19; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 4 GCTCTAGAATGAACGGTGG 22

RESULT 4
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; TITLE OF INVENTION: TELOMERASE ASSAY OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 100.0%; Score 19; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 4 GCTCTAGAATGAACGGTGG 22

RESULT 5
PCT-US96-14679-27
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```
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 6
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US96-14679A-27

Query Match          100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
   |||||
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 7
PCT-US99-03302-4
; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; FILE REFERENCE: 1489JS 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3C,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match          100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
   |||||
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 8
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
   |||||
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 9
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
   |||||
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 10
US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-08-387-524-19
; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-387-524-19

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

US-08-387-524-19
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-524-19

Query Match 100.0%; Score 19; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
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RESULT 13
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 14
US-08-482-115A-23
; Sequence 23, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115A-23

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 15
US-08-520-550-19
; Sequence 19, Application US/08520550
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-520-550-19

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Query Match      100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGAAATGAACGGTGG 19
         |||||
Db      5 GCTCTAGAAATGAACGGTGG 23

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Search completed: June 25, 2003, 06:20:26
Job time : 1612.81 secs

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REGISTRATION NUMBER: 00 00/011,112
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 5 GCTCTAGATGACGGTGG 23

RESULT 2

US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 5 GCTCTAGATGACGGTGG 23

RESULT 3

US-09-057-351-23

Sequence 23, Application US/09057351

Patent No. US20010034439A1

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,351

FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000821US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 19; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 4
US-10-098-263B-64498/c
; Sequence 64498, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match 72.6%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCTAGATGAACGGTGG 19
|||||
Db 23 TCTAGATGAACGGTGG 7

RESULT 5
US-10-139-483-3
; Sequence 3, Application US/10139483
; Publication No. US20030055266A1
; GENERAL INFORMATION:
; APPLICANT: Beeley, Nigel R
; APPLICANT: Behan, Dominic P
; APPLICANT: Chalmers, Derek T
; APPLICANT: Menzaghi, Frederique
; APPLICANT: Strah-Pleyvet, Sonja
; TITLE OF INVENTION: Small Molecule Modulators Of G Protein-Coupled Receptor
; TITLE OF INVENTION: Six
; FILE REFERENCE: AREN0058
; CURRENT APPLICATION NUMBER: US/10/139,483
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/513,838
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/364,425
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-139-483-3

Query Match 72.6%; Score 13.8; DB 9; Length 31;
Best Local Similarity 88.2%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTCTAGATGAACGGTG 18
|||||
Db 4 CTCTAGATGCGGGTG 20

RESULT 6
US-10-098-263B-51583
; Sequence 51583, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-51583

Query Match 69.5%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCTAGATGAACGGTGG 19
|||||
Db 7 CTCTAGATCAACGGTGG 24

RESULT 7
US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer
US-09-952-522B-19

Query Match 69.5%; Score 13.2; DB 9; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTG 18
|||||

Db 1 GCTCTAGATGAAGACTG 18

RESULT 8

US-10-090-182A-255

; Sequence 255, Application US/10090182A

; Publication No. US20030103936A1

; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

Bauer, S. C.

Braford-Goldberg, Sarah R.

Caparon, Mairé H.

Easton, Alan M.

Klein, Barbara K.

McKearn, John P.

Olin, Peter O.

Paik, Kuman

Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of

Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple

Mutation Polypeptides

NUMBER OF SEQUENCES: 415

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corp

Corporate Patent Dept. Mail Zone 04E

STREET: 800 N. Lindbergh Blvd.

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/090,182A

FILING DATE: 03-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/764,114

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 07/981,044

FILING DATE: 24-NOV-1992

APPLICATION NUMBER: PCT/US93/11197

FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 08/411,795

FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C2713/12

TELECOMMUNICATION INFORMATION:

TELEPHONE: (636)737-6257

TELEFAX: (736)737-6257

INFORMATION FOR SEQ ID NO: 255:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

SEQUENCE DESCRIPTION: SEQ ID NO: 255:

US-10-090-182A-255

Query Match 69.5%; Score 13.2; DB 9; Length 40;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAAGACTG 18

Db 12 GCTCTATAATGATCGATG 29

RESULT 9

US-10-090-182A-234

; Sequence 234, Application US/10090182A

; Publication No. US20030103936A1

; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

Bauer, S. C.

Braford-Goldberg, Sarah R.

Caparon, Mairé H.

Easton, Alan M.

Klein, Barbara K.

McKearn, John P.

Olin, Peter O.

Paik, Kuman

Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of

Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple

Mutation Polypeptides

NUMBER OF SEQUENCES: 415

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corp

Corporate Patent Dept. Mail Zone 04E

STREET: 800 N. Lindbergh Blvd.

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/090,182A

FILING DATE: 03-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/764,114

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 07/981,044

FILING DATE: 24-NOV-1992

APPLICATION NUMBER: PCT/US93/11197

FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 08/411,795

FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C2713/12

TELECOMMUNICATION INFORMATION:

TELEPHONE: (636)737-6257

TELEFAX: (736)737-6257

INFORMATION FOR SEQ ID NO: 234:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

SEQUENCE DESCRIPTION: SEQ ID NO: 234:

US-10-090-182A-234

Query Match 69.5%; Score 13.2; DB 9; Length 41;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAAGACTG 18

Db 12 GCTCTATAATGATCGATG 29

RESULT 10

US-10-090-182A-235/c
; Sequence 235, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Oline, Peter O.
; Paik, Kuman
; Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELEPHONE: (636)737-6257
TELEFAX: (736)737-6257

INFORMATION FOR SEQ ID NO: 235:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)

SEQUENCE DESCRIPTION: SEQ ID NO: 235:
US-10-090-182A-235

Query Match 69.5%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTG 18
Db 38 GCTCTATAATGATCGATG 21

RESULT 11
US-10-090-182A-409/c
; Sequence 409, Application US/10090182A

Publication No. US20030103936A1
; GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Oline, Peter O.
; Paik, Kuman
; Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELEPHONE: (636)737-6257
TELEFAX: (736)737-6257

INFORMATION FOR SEQ ID NO: 409:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 409:
US-10-090-182A-409

Query Match 69.5%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTG 18
Db 38 GCTCTATAATGATCGATG 21

RESULT 12
US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

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; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-098-263B-118949

Query Match      68.4%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAACG 15
Db 20 TCTAGATGAACG 8

RESULT 13
US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match      68.4%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAA 13
Db 1 GCTCTAGATGAA 13

RESULT 14
US-10-215-112-12114/c
; Sequence 12114, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 12114
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12114
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Query Match      67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 GCTCTAGATGAACGG 16
Db 21 GCTCTAGATGAACGG 6
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RESULT 15
US-10-215-112-12846
; Sequence 12846, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12846
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Query Match      67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4 CTAGATGAACGGTGG 19
Db 5 CTCGATGAACGGTGG 20
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Search completed: June 25, 2003, 22:25:07
Job time : 58.757 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 28.8406 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	2	US-08-770-565-9
2	19	100.0	26	1	US-08-330-123A-23
3	19	100.0	26	1	US-08-482-115B-23
4	19	100.0	26	2	US-08-660-678A-23
5	19	100.0	26	2	US-08-710-249-26
6	19	100.0	26	2	US-08-485-778-19
7	19	100.0	26	2	US-08-472-802C-24
8	19	100.0	26	3	US-08-520-550A-19
9	19	100.0	26	3	US-08-998-443-23
10	19	100.0	26	4	US-08-974-549A-598
11	19	100.0	26	4	US-08-060-523-23
12	19	100.0	26	4	US-08-220-157A-26
13	19	100.0	26	4	US-08-286-959B-4
14	19	100.0	26	4	US-08-580-517-23
15	19	100.0	27	2	US-08-770-565-26
16	19	100.0	30	2	US-08-770-565-8
17	18	94.7	30	2	US-08-833-377-6
18	16.4	86.3	18	4	US-08-974-549A-543
19	15.8	83.2	27	3	US-08-630-172-24
20	15.8	83.2	27	4	US-08-375-419-24
21	15.4	81.1	42	1	US-08-439-813-2
22	15.4	81.1	42	5	PCT-US96-05291A-2
23	15	78.9	15	2	US-08-770-565-10
24	13.8	72.6	31	4	US-08-513-838-3
25	13.2	69.5	40	1	US-08-411-795B-255
26	13.2	69.5	40	1	US-08-469-319A-255
27	13.2	69.5	40	4	US-08-764-114-255

Sequence 255, App
Sequence 234, App
Sequence 234, App
Sequence 234, App
Sequence 234, App
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Sequence 235, App
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Sequence 409, App
Sequence 235, App
Sequence 235, App
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Sequence 235, App
Sequence 409, App
Sequence 235, App
Sequence 9, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl

28 13.2 69.5 40 4 US-08-469-419-255
29 13.2 69.5 41 1 US-08-411-795B-234
30 13.2 69.5 41 1 US-08-469-319A-234
31 13.2 69.5 41 4 US-08-764-114-234
32 13.2 69.5 41 4 US-08-469-419-234
33 13.2 69.5 45 1 US-08-411-795B-235
34 13.2 69.5 45 1 US-08-411-795B-409
35 13.2 69.5 45 1 US-08-469-319A-235
36 13.2 69.5 45 1 US-08-469-319A-409
37 13.2 69.5 45 4 US-08-764-114-235
38 13.2 69.5 45 4 US-08-764-114-409
39 13.2 69.5 45 4 US-08-469-419-235
40 13.2 69.5 45 4 US-08-469-419-409
41 12.8 67.4 48 2 US-08-729-955A-9
42 12.4 65.3 23 4 US-09-273-839A-3
43 12.4 65.3 25 2 US-08-813-940-12
44 12.4 65.3 26 1 US-08-480-604A-16
45 12.4 65.3 26 2 US-08-405-496A-16

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GCTCTAGATGAACGGTGG 19

```
Db      1 GCTCTAGAAATGAACGGTGG 19
|||||
RESULT 2
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match      100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
|||||
Db      5 GCTCTAGAAATGAACGGTGG 23
|||||

RESULT 4
US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-000811US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-660-678A-23

Query Match 100.0%; Score 19; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 5

US-08-710-249-26
 ; Sequence 26, Application US/08710249
 ; Patent No. 5858777
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Andrews, William H.
 ; APPLICANT: Adams, Robert R.
 ; TITLE OF INVENTION: Methods and Reagents for Regulating
 ; TITLE OF INVENTION: Telomere Length and Telomerase Activity
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/710,249
 ; FILING DATE: 13-SEP-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/583,808
 ; FILING DATE: 05-JAN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/003,492
 ; FILING DATE: 08-SEP-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-001220US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-710-249-26
 Query Match 100.0%; Score 19; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 6

US-08-485-778-19
 ; Sequence 19, Application US/08485778
 ; Patent No. 5876979
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrews, William H.
 ; APPLICANT: Avilion, Ariel Athena
 ; APPLICANT: Peng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Greider, Carol
 ; APPLICANT: Marhuenda, Maria Antonia Blasco
 ; APPLICANT: Villeponteau, Bryant
 ; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,778
 ; FILING DATE: 07-JE-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/387,524
 ; FILING DATE: 13-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL94-05A4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-485-778-19

Query Match 100.0%; Score 19; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-08-520-550A-19
US-08-520-550A-19, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillon, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

```

/ / GENERAL INFORMATION:
/ / APPLICANT: Villeponteau, Bryant
/ / APPLICANT: Feng, Junli
/ / APPLICANT: Funk, Walter
/ / APPLICANT: Andrews, William H.
/ / TITLE OF INVENTION: Mammalian Telomerase
/ / NUMBER OF SEQUENCES: 30
/ / CORRESPONDENCE ADDRESS:
/ / ADDRESSEE: Townsend and Townsend and C
/ / STREET: Two Embarcadero Center, Eighth
/ / CITY: San Francisco
/ / STATE: California
/ / COUNTRY: USA
/ / ZIP: 94111-3834
/ / COMPUTER READABLE FORM:
/ / MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-998-443-23

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-08-974-549A-598
; Sequence 598, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
;
US-08-974-549A-598

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-09-060-523-23
; Sequence 23, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
```

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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-060-523-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-09-220-157A-26
; Sequence 26, Application US/09220157A
; Patent No. 6300110
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; NUMBER OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-220-157A-26

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 13
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-286-959B-4

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 14
US-09-580-517-23
; Sequence 23, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; FUNK, Junli
; FUNK, Walter

```

ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 15

US-08-770-565-26
Sequence 26, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-26

Query Match 100.0%; Score 19; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

Search completed: June 25, 2003, 00:24:39
Job time : 28.8406 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 979.598 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table: OLIGO NUC
Gapop_60.0, Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

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2: em_esthum:*
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9: gb_est1:*
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13: gb_est4:*
14: gb_est5:*
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25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	11	57.9	48	17	AZ606694
2	10	52.6	19	17	AZ471573
3	10	52.6	28	17	TA116B03P
4	10	52.6	29	17	TA264G10Q
5	10	52.6	34	10	AV964763
6	10	52.6	46	9	AA681423
					AA681423 vr41f08.s

7	10	52.6	49	17	BH791685
8	9	47.4	22	9	AU259636
9	9	47.4	24	17	AZ662500
10	9	47.4	25	9	AU763346
11	9	47.4	25	9	WI55D06.X
12	9	47.4	27	9	AU254302
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14	9	47.4	27	17	BH849811
15	9	47.4	27	17	TA349802P
16	9	47.4	30	9	AU257604
17	9	47.4	31	9	AI032592
18	9	47.4	31	17	TA106A06P
19	9	47.4	34	12	BG339578
20	9	47.4	34	12	BG340055
21	9	47.4	34	17	TA182F12P
22	9	47.4	36	12	BE797241
23	9	47.4	36	17	AZ812974
24	9	47.4	38	17	AZ786040
25	9	47.4	40	12	BG563012
26	9	47.4	41	9	AU258962
27	9	47.4	41	17	AZ775318
28	9	47.4	41	17	BH863752
29	9	47.4	41	17	BH863753
30	9	47.4	41	17	BH864990
31	9	47.4	42	12	BF732142
32	9	47.4	42	12	BG613445
33	9	47.4	42	14	CO1062
34	9	47.4	43	9	AA445326
35	9	47.4	43	17	AZ456311
36	9	47.4	44	17	AZ435397
37	9	47.4	44	17	BH624958
38	9	47.4	44	17	AL757115
39	9	47.4	45	17	AQ026252
40	9	47.4	46	17	AZ812338
41	9	47.4	46	17	AL771310
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43	9	47.4	46	17	TA352805Q
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45	9	47.4	48	17	AZ831830
			49	10	AW100845

ALIGNMENTS

RESULT 1
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LOCUS IM0428D15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0428D15 R, DNA sequence.
ACCESSION AZ606694
VERSION AZ606694.1 GI:11728884
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 48)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Telam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

48 bp DNA linear GSS 13-DEC-2000
AZ606694 IM0428D15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0428D15 R, DNA sequence.

ACCESSION AZ606694

VERSION AZ606694.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 48)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Telam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0428 row: D column: 15
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 48.

FEATURES

source

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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0428D15"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 13 c 15 g 10 t
 ORIGIN

Query Match 57.9%; Score 11; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGG 19
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 Db 38 ATGAACGGTGG 48

RESULT 2

AZ471573/c

LOCUS

AZ471573 19 bp DNA linear GSS 04-OCT-2000
 IM0286G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0286G13 F, DNA sequence.

ACCESSION

AZ471573
 A2471573.1 GI:10629698

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

plasmid inserts

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0286 row: G column: 13
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1. 19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286G13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 3 c 6 g 4 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGATG 11
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 Db 15 CTCTAGATG 6

RESULT 3

TA116E03P

LOCUS

TA116E03P 28 bp DNA linear GSS 13-DEC-2000
 T. brucei sheared genomic DNA clone 116e03, forward sequence,
 genomic survey sequence.

ACCESSION

AL462526
 AL462526.1 GI:11832364

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei.

ORGANISM

Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 28)

REFERENCE

1 (bases 1 to 28)

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajadream, M.A. and Barrell, B.G.

TITLE

Direct Submission

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
Email: neilsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .28
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="116e03"

BASE COUNT 7 a 5 c 8 g 8 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAATGAACGG 16

Db 2 GAATGAACGG 11

RESULT 4

TA264G10Q 29 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 264g10, reverse sequence,
genomic survey sequence.

ACCESSION AL487013

VERSION AL487013.1 GI:11850630

KEYWORDS GSS.

SOURCE

ORGANISM

Trypanosoma brucei.

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 29)

Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,

Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,

Meiville S.E., Rajandream M.A. and Barrell B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: neilsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .29
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="264g10"

BASE COUNT 11 a 5 c 11 g 2 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 29;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAACG 15

Db 7 AGAATGAACG 16

RESULT 5

AV964763/c

LOCUS

DEFINITION

intestinalis cDNA clone ciad15006 5', mRNA sequence.

ACCESSION

AV964763

VERSION

AV964763.1 GI:19454459

KEYWORDS

EST.

SOURCE

ORGANISM

Ciona intestinalis.

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 34)

Sato N., Satou Y., Kohara Y. and Shin-i T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Sato

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: sato@secidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. .34

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="ciad15006"

/clone_lib="Nori Sato unpublished cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/notes="Vector: pBluescript SK"

BASE COUNT 12 a 5 c 8 g 9 t

ORIGIN

Query Match 52.6%; Score 10; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAT 10

Db 16 GCTCTAGAAT 7

RESULT 6

AA681423/c

LOCUS

DEFINITION

vr41f08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

IMAGE:1123239 5', similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A

(HUMAN); mRNA sequence.

ACCESSION

AA681423

VERSION

AA681423.1 GI:2663563

KEYWORDS

EST.

SOURCE

house mouse.

Mus musculus

Location/Qualifiers

1 (bases 1 to 46)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)

Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,

Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,

Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,

Theising B., Wylie T., Lennon G., Soares B., Wilson R. and

Waterston R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

AV964763 34 bp mRNA linear EST 14-MAR-2002
AV964763 Nori Sato unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad15006 5', mRNA sequence.

AV964763.1 GI:19454459

EST.

Ciona intestinalis.

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 34)

Sato N., Satou Y., Kohara Y. and Shin-i T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Sato

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: sato@secidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. .34

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="ciad15006"

/clone_lib="Nori Sato unpublished cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/notes="Vector: pBluescript SK"

BASE COUNT 12 a 5 c 8 g 9 t

ORIGIN

Query Match 52.6%; Score 10; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAT 10

Db 16 GCTCTAGAAT 7

AA681423 46 bp mRNA linear EST 05-DEC-1997
vr41f08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:1123239 5', similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A
(HUMAN); mRNA sequence.

AA681423

VERSION

AA681423.1 GI:2663563

KEYWORDS

EST.

SOURCE

house mouse.

Mus musculus

Location/Qualifiers

1 (bases 1 to 46)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)

Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,

Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,

Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,

Theising B., Wylie T., Lennon G., Soares B., Wilson R. and

Waterston R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:612575

Trace considered overall poor quality

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1. .46
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE.1123239"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"

/note="Organ: embryo; Vector: pBluescribe (modified); Site 1: Mui1; Site 2: Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: Sal1 (5'-CGGTGACCGTCGCGTTTCTTTT-3', cDNAs were cloned into the Mui1/Sal1 sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

BASE COUNT 13 a 19 c 7 g 7 t

ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGAACGGTGG 19

Db 17 TGAACGGTGG 8

RESULT 7

BH791685

LOCUS

DEFINITION BH791685 49 bp DNA linear GSS 02-APR-2002
SALK_060837.45.60.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_060837.45.60.x, DNA sequence.

ACCESSION BH791685

VERSION BH791685.1

KEYWORDS GI:19885809

SOURCE GSS.

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 49)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1. .49

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_060837.45.60.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT

ORIGIN 15 a 9 c 9 g 16 t

Query Match 52.6%; Score 10; DB 17; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAAT 10

Db 39 GCTCTAGAAAT 48

RESULT 8

LOCUS AU259636

DEFINITION AU259636 22 bp mRNA linear EST 25-APR-2002

3'-directed mouse cDNA library Mus musculus cDNA clone

RED0015510 3', mRNA sequence.

ACCESSION AU259636

VERSION AU259636.1

KEYWORDS GI:20326342

SOURCE EST.

ORGANISM house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Kato,K. and Matoba,R.

Generation of expressed sequence tags from mouse brain

Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@b.ais-t-nara.ac.jp,

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="BED0015510"

/clone_lib="3'-directed mouse cDNA library"

/tissue_type="brain"

/note="Vector: pGEM-T-easy"

BASE COUNT 13 a 3 c 4 g 2 t

ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAAC 14

Db 11 AGAATGAAC 19

RESULT 9

AZ662500

LOCUS AZ662500

DEFINITION AZ662500 24 bp DNA linear GSS 14-DEC-2000

1M0541G07R Mouse 10kb plasmid UUGClM library Mus musculus genomic

clone UUGClM0541G07 R, DNA sequence.

ACCESSION AZ662500

VERSION AZ662500.1

KEYWORDS GI:11799646

SOURCE GSS.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
        ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
        University of Utah Genome Center
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0541 row: G column: 07
        Seq primer: CACACGGAACACCTATGACC
        Class: plasmid ends
        High quality sequence stop: 24.
FEATURES source
        1. .24
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db xref="taxon:10090"
        /clone="UUGC1M0541G07"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /notes="vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        ligated DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|47332114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adapted vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
BASE COUNT 8 a 3 c 7 g 6 t
ORIGIN
        Query Match 47.4%; Score 9; DB 17; Length 24;
        Best Local Similarity 100.0%; Pred. No. 1.5e+05;
        Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGAACGGTG 18
    |||||
Db 16 TGAACGGTG 24

RESULT 10
AI763346 25 bp mRNA linear EST 21-DEC-1999
LOCUS w155D06.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2394155 3'
DEFINITION Similar to TR:O75053 KIAA0465 PROTEIN ;, mRNA sequence.
ACCESSION AI763346
VERSION AI763346
KEYWORDS AI763346.1 GI:5179013
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        JOURNAL
        COMMENT

```

```

REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgapsb@nci.nih.gov
        Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
        , Ph.D.
        cDNA Library Preparation: M. Bento Soares, Ph.D.
        cDNA Library Arrayed by: Greg Lennon, Ph.D.
        DNA Sequencing by: Washington University Genome Sequencing Center
        Clone distribution: NCI-CGAP clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        www.bio.llnl.gov/bbrp/image/image.html
        Insert Length: 1675 Std Error: 0.00
        Seq primer: -40UP from Gibco
        High quality sequence stop: 1.
FEATURES source
        1. .25
        /organism="Homo sapiens"
        /db xref="taxon:9606"
        /clone="IMAGE:2394155"
        /clone_lib="NCI CGAP Col6"
        /tissue_type="colon tumor, RER+"
        /lab_host="DH10B"
        /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
        modified polylinker; Site 1: Not 1; Site 2: Eco RI;
        Plasmid DNA from the normalized library NCI-CGAP Col6 was
        prepared, and ss circles were made in vitro. Following HAP
        purification, this DNA was used as tracer in a subtractive
        hybridization reaction. The driver was PCR-amplified cDNAs
        from a pool of 5,000 clones made from the same library
        (clones IDs 1057416-1061255, and 1144584-1145351).
        Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 9 a 3 c 7 g 6 t
ORIGIN
        Query Match 47.4%; Score 9; DB 9; Length 25;
        Best Local Similarity 100.0%; Pred. No. 1.6e+05;
        Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTAGAATGA 12
    |||||
Db 12 CTAGAATGA 20

RESULT 11
AU254302/c 27 bp mRNA linear EST 25-APR-2002
LOCUS AU254302 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0001498 3', mRNA sequence.
ACCESSION AU254302
VERSION AU254302.1 GI:20315955
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
        JOURNAL
        COMMENT
        Contact: Kikuya Kato
        Graduate School of Biological Sciences
        Nara Institute of Science and Technology
        8916-5 Takayama, Ikoma, Nara 630-0101, Japan
        Tel: 81-743-72-5581
        Fax: 81-743-72-5589
        Email: kkatob@bs.aist-nara.ac.jp,
        URL:http://love2.aist-nara.ac.jp/BED/index.html.
        Location/Qualifiers
        1. .27
        source

```

RESULT 12
BH812447
LOCUS
DEFINITION
/organism="Mus musculus"
/db xref="taxon:10090"
/clone="BBD0001498"
/clone_lib="3'-directed mouse cDNA library"
/tissue_types="brain"
/note="vector: pGEM-T-easy"
11 a 3 c 4 g 9 t

Query Match 47.4%; Score 9; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGAATGAA 13
|||||
DB 25 TAGAATGAA 17

RESULT 13
BH849811
LOCUS
DEFINITION
/organism="Arabidopsis thaliana"
/db xref="taxon:10090"
/clone="SALK_070310.38.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/tissue_types="root"
/note="vector: pGEM-T-easy"
27 bp DNA linear GSS 02-MAY-2002
SALK_070310.38.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_061781, DNA sequence.

ACCESSION
BH812447
VERSION
BH812447.1 GI:20390902
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 27)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

FEATURES
source
Location/Qualifiers
1..27
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK_061781"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
12 a 3 c 5 g 7 t

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAA 10
|||||
DB 18 CTCTAGAA 26

RESULT 14
TA349B02P
LOCUS
DEFINITION
/organism="Trypanosoma brucei"
/db xref="taxon:3702"
/clone="SALK_061781"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
27 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 349b02, forward sequence,
genomic survey sequence.

ACCESSION
AL493641
VERSION
AL493641.1 GI:11869420
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAA 11
|||||
DB 8 TCTAGAA 16

RESULT 15
TA349B02P
LOCUS
DEFINITION
/organism="Trypanosoma brucei"
/db xref="taxon:3702"
/clone="SALK_061781"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
27 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 349b02, forward sequence,
genomic survey sequence.

RESULT 13
BH849811
LOCUS
DEFINITION

ACCESSION
BH849811
VERSION
BH849811.1 GI:21420682
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 27)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

FEATURES
source
Location/Qualifiers
1..27
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK_070310.38.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
7 a 2 c 8 g 10 t

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAA 11
|||||
DB 8 TCTAGAA 16

RESULT 14
TA349B02P
LOCUS
DEFINITION

ACCESSION
AL493641
VERSION
AL493641.1 GI:11869420
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAA 11
|||||
DB 8 TCTAGAA 16

RESULT 15
TA349B02P
LOCUS
DEFINITION

ACCESSION
AL493641
VERSION
AL493641.1 GI:11869420
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAA 11
|||||
DB 8 TCTAGAA 16

RESULT 16
TA349B02P
LOCUS
DEFINITION

ACCESSION
AL493641
VERSION
AL493641.1 GI:11869420
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission

BASE COUNT
ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .27
Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="349b02"

BASE COUNT

4 a 10 c 8 g 5 t

ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAA 9

|||||
Db 7 GCTCTAGAA 15

RESULT 15

AU257604

LOCUS

AU257604 30 bp mRNA linear EST 25-APR-2002
AU257604 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0011024 3', mRNA sequence.

ACCESSION

AU257604

VERSION

AU257604.1 GI:20322387

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 30)

AUTHORS

Kato, K. and Matoba, R.

TITLE

Generation of expressed sequence tags from mouse brain

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@bs.aist-nara.ac.jp,
URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1. .30
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0011024"
/clone_lib="3'-directed mouse cDNA library"
/tissue type="brain"
/note="Vector: pGEM-T-easy"

BASE COUNT

13 a 6 c 4 g 7 t

ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAA 10
|||||
Db 5 CTCTAGAA 13

Search completed: June 23, 2003, 10:10:26
Job time : 981.752 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 834.032 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table:
OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*
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2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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8: /cgn2_6/ptodata/1/pna/US13_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US17_NEW_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	19	100.0	21	1	PCT-US03-04088-543
C 3	19	100.0	21	1	PCT-US03-04088-547
C 4	19	100.0	21	1	PCT-US03-04088-551
C 5	19	100.0	21	1	PCT-US03-04088-555
C 6	19	100.0	21	1	PCT-US03-04088-559
C 7	19	100.0	23	1	PCT-US03-04088-520
C 8	19	100.0	23	1	PCT-US03-04088-521
C 9	19	100.0	26	6	US-09-721-456-598
C 10	19	100.0	26	9	US-10-325-810-598
C 11	19	100.0	26	9	US-10-359-935-23
C 12	19	100.0	30	10	US-10-330-872-5
C 13	19	100.0	30	10	US-10-330-872A-5
C 14	17	89.5	21	1	PCT-US03-04088-538
C 15	17	89.5	21	1	PCT-US03-04088-542
C 16	17	89.5	21	1	PCT-US03-04088-546
C 17	17	89.5	21	1	PCT-US03-04088-550
C 18	17	89.5	21	1	PCT-US03-04088-554
C 19	17	89.5	21	1	PCT-US03-04088-558
C 20	14	73.7	23	9	US-10-310-188-36216

21	14	73.7	24	8	US-10-442-506-39	Sequence 39, Appl
22	14	73.7	25	12	US-60-427-808-952738	Sequence 952738, A
23	14	73.7	25	13	US-60-469-545-13722	Sequence 13722, A
C 24	14	73.7	25	13	US-60-469-545-222991	Sequence 222991, A
25	13	68.4	18	6	US-09-721-456-543	Sequence 543, App
26	13	68.4	18	9	US-10-325-810-543	Sequence 543, App
C 27	13	68.4	25	6	US-09-660-222-3845	Sequence 3845, App
C 28	13	68.4	25	6	US-09-660-222-3846	Sequence 3846, App
C 29	13	68.4	25	6	US-09-660-222-3854	Sequence 3854, App
C 30	13	68.4	25	9	US-10-098-263B-118949	Sequence 118949, A
C 31	13	68.4	25	9	US-10-355-577-90268	Sequence 90268, A
C 32	13	68.4	25	9	US-10-355-577-173196	Sequence 173196, A
C 33	13	68.4	25	9	US-10-355-577-231533	Sequence 231533, A
C 34	13	68.4	25	12	US-60-427-836-69383	Sequence 69383, A
C 35	13	68.4	25	12	US-60-427-836-69383	Sequence 69383, A
C 36	13	68.4	25	12	US-60-427-836-267834	Sequence 267834, A
C 37	12	63.2	25	6	US-09-660-222-29735	Sequence 29735, A
C 38	12	63.2	25	7	US-09-954-445A-17344	Sequence 17344, A
C 39	12	63.2	25	7	US-09-954-445A-17345	Sequence 17345, A
C 40	12	63.2	25	7	US-09-954-445A-46246	Sequence 46246, A
C 41	12	63.2	25	7	US-09-954-445A-46248	Sequence 46248, A
C 42	12	63.2	25	7	US-09-954-445A-84990	Sequence 84990, A
C 43	12	63.2	25	9	US-10-098-263B-64498	Sequence 64498, A
C 44	12	63.2	25	9	US-10-355-577-2113	Sequence 2113, App
C 45	12	63.2	25	9	US-10-355-577-42242	Sequence 42242, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-539/C
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 19; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 19 GCTCTAGAAATGAACGGTGG 1

RESULT 2
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(11)
; OTHER INFORMATION: 5'-3' attached terminal deoxybasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 19 GCTCTAGAAATGAACGGTGG 1

RESULT 4
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 1 GCUCUAGAUGAACGGUGG 19

RESULT 3
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
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```

; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-551

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. NO. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 1 GCUCUAGAUGAACGGUGG 19

RESULT 5
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

```

NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 19 GCTCTAGATGAACGGTGG 1

RESULT 6

PCT-US03-04088-559
Sequence 559, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 559
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(5)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6)..(9)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)..(10)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature

LOCATION: (14)..(14)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 1 GCUCUAGUAUGAACGGUGG 19

RESULT 7

PCT-US03-04088-520/c
Sequence 520, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 520
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 100.0%; Score 19; DB 1; Length 23;

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Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 23 GCTCTAGATGAACGGTGG 5

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 521
; TYPE: RNA
; LENGTH: 23
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 100.0%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 21 GCTCTAGATGAACGGTGG 3

RESULT 9
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /notes "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
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US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Viliepointeau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598
Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 11
US-10-325-810-598
Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 11

US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Viliepointeau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23
Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 12
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C

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; CURRENT APPLICATION NUMBER: US/10/330,872
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5
Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5
Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)...(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-538
Query Match      89.5%; Score 17; DB 1; Length 21;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 542, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15

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; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-542

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Query Match      89.5%  Score 17; DB 1; Length 21;
Best Local Similarity 76.5%  Pred.No. 1.7;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Search completed: June 23, 2003, 19:12:12
Job time : 834.032 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1593.58 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGAAATGAACGGCTGG 19

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	19	100.0	19	11	US-08-770-564A-9 Sequence 4, Appli
3	19	100.0	25	16	US-09-250-336A-4 Sequence 4, Appli
4	19	100.0	25	25	US-09-642-177-4 Sequence 27, Appli
5	19	100.0	26	1	PCT-US96-14679-27 Sequence 27, Appli
6	19	100.0	26	1	PCT-US96-14679A-27 Sequence 4, Appli
7	19	100.0	26	1	PCT-US99-03302-4 Sequence 4, Appli
8	19	100.0	26	1	PCT-US99-07533-4 Sequence 4, Appli
9	19	100.0	26	1	PCT-US99-07533-4 Sequence 23, Appli
10	19	100.0	26	6	US-08-272-102-23 Sequence 19, Appli
11	19	100.0	26	7	US-08-387-524-19 Sequence 24, Appli
12	19	100.0	26	8	US-08-472-802A-24 Sequence 24, Appli
13	19	100.0	26	8	US-08-472-802B-24 Sequence 23, Appli
14	19	100.0	26	8	US-08-482-115A-23 Sequence 19, Appli
15	19	100.0	26	9	US-08-520-550-19 Sequence 41, Appli
16	19	100.0	26	9	US-08-521-634-41 Sequence 23, Appli
17	19	100.0	26	10	US-08-660-678-23 Sequence 23, Appli
18	19	100.0	26	13	US-08-911-312-23 Sequence 23, Appli
19	19	100.0	26	13	US-08-911-312A-23 Sequence 312, Appli
20	19	100.0	26	13	US-08-913-951-312 Sequence 17, Appli
21	19	100.0	26	13	US-08-973-589-17

Sequence 598, App
Sequence 23, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 45, Appl
Sequence 598, App
Sequence 598, App
Sequence 5, Appl
Sequence 598, App
Sequence 598, App
Sequence 9, Appl
Sequence 26, Appl
Sequence 312, App
Sequence 312, App
Sequence 26, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US97-23619-9
; Sequence 9, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note="oligo 21ab"
PCT-US97-23619-9

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 1 GCTCTAGATGAACGGTGG 19

RESULT 2
US-08-770-564A-9
; Sequence 9, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-9

Query Match 100.0%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 1 GCTCTAGATGAACGGTGG 19

RESULT 3
US-09-250-336A-4

; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; CURRENT FILING DATE: 1999-02-16
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 100.0%; Score 19; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 4 GCTCTAGATGAACGGTGG 22

RESULT 4
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 100.0%; Score 19; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 4 GCTCTAGATGAACGGTGG 22

RESULT 5
PCT-US96-14679-27

; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 6
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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1  RESULT 10
2  US-08-272-102-23
3  ; Sequence 23, Application US/08272102
4  ; GENERAL INFORMATION:
5  ; APPLICANT: VILLEPONTEAU, Bryant
6  ; APPLICANT: FENG, Junli
7  ; APPLICANT: FUNK, Walter
8  ; APPLICANT: ANDREWS, William H.
9  ; TITLE OF INVENTION: HUMAN TELOMERASE
10 ; NUMBER OF SEQUENCES: 24
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESS: Townsend and Townsend Khourie and Crew
13 ; STREET: 379 Lytton Avenue
14 ; CITY: Palo Alto
15 ; STATE: California
16 ; COUNTRY: US
17 ; ZIP: 94301
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0. Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-08-387-524-19
; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match          100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-524-19

Query Match          100.0%; Score 19; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match          100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
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RESULT 13
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 14
US-08-482-115A-23
; Sequence 23, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-23

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 15
US-08-520-550-19
; Sequence 19, Application US/08520550
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550-19

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Query Match      100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGATGAACGGTGG 19
Db      5 GCTCTAGATGAACGGTGG 23

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Search completed: June 23, 2003, 16:08:21
Job time : 1593.65 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 152.681 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGACGGTGG 19

Scoring table:

OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	26	9	US-10-044-692-312
2	19	100.0	26	9	US-10-044-539-312
3	19	100.0	26	10	US-09-057-351-23
4	13	68.4	25	9	US-10-098-263B-118949
5	13	68.4	26	9	US-09-352-522B-19
6	13	68.4	28	10	US-09-844-006A-3
7	12	63.2	23	9	US-09-952-522B-17
8	12	63.2	23	9	US-09-952-522B-31
9	12	63.2	25	9	US-10-215-112-6862
10	12	63.2	25	9	US-10-098-263B-64498
11	12	63.2	26	9	US-10-011-366-16
12	11	57.9	17	10	US-09-969-373-1959
13	11	57.9	21	9	US-09-997-868-13
14	11	57.9	22	10	US-09-765-873A-5
15	11	57.9	23	9	US-09-952-522B-9
16	11	57.9	24	9	US-09-754-853A-676
17	11	57.9	24	9	US-10-245-813-2
18	11	57.9	25	9	US-10-098-263B-10750
19	11	57.9	25	9	US-10-098-263B-22667

ALIGNMENTS

RESULT 1

US-10-044-692-312

; Sequence 312, Application US/10044692

; Publication No. US20030096344A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/044,692

; FILING DATE: 11-Jan-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/912,951

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 2
US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 3
US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villegonteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 19; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 4

US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittleman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match 68.4%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15
|||||
Db 20 TCTAGAAATGAACG 8

RESULT 5

US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer

US-09-952-522B-19

Query Match 68.4%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 6

US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match 68.4%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 7

US-09-952-522B-17
; Sequence 17, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 23

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/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
/ OTHER INFORMATION: forward primer
US-09-952-522B-17

Query Match      63.2%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGA 12
   |||||
Db 1 GCTCTAGAATGA 12

RESULT 8
US-09-952-522B-31
/ Sequence 31, Application US/09952522B
/ Publication No. US20030082152A1
/ GENERAL INFORMATION:
/ APPLICANT: Katz, Adam J.
/ APPLICANT: Lluil, Ramon
/ APPLICANT: Futrell, J. William
/ APPLICANT: Hedrick, Marc H.
/ APPLICANT: Benhaim, Prosper
/ APPLICANT: Lorenz, Hermann Peter
/ APPLICANT: Zhu, Min
/ TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
/ FILE REFERENCE: 30448.77US11
/ CURRENT APPLICATION NUMBER: US/09/952,522B
/ CURRENT FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: PCT/US00/06232
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: 60/123,711
/ PRIOR FILING DATE: 1999-03-10
/ PRIOR APPLICATION NUMBER: 60/162,462
/ PRIOR FILING DATE: 1999-10-29
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 31
/ LENGTH: 23
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
/ OTHER INFORMATION: forward primer
US-09-952-522B-31

Query Match      63.2%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGA 12
   |||||
Db 1 GCTCTAGAATGA 12

RESULT 9
US-10-215-112-6862/c
/ Sequence 6862, Application US/10215112
/ Publication No. US20030082596A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Wittmann
/ TITLE OF INVENTION: Method of Genetic Analysis of Probes:
/ FILE REFERENCE: 3119
/ CURRENT APPLICATION NUMBER: US/10/215,112
/ CURRENT FILING DATE: 2002-08-08
/ NUMBER OF SEQ ID NOS: 14936
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6862
/ LENGTH: 25
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/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6862

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGA 12
   |||||
Db 15 GCTCTAGAATGA 4

RESULT 10
US-10-098-263B-64498/c
/ Sequence 64498, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Mittman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 64498
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAATGAAC 14
   |||||
Db 23 TCTAGAATGAAC 12

RESULT 11
US-10-011-366-16
/ Sequence 16, Application US/10011366
/ Publication No. US20030054493A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, James A.
/ APPLICANT: Kink, John A.
/ TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
/ OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
/ DISEASE
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Medlen & Carroll
/ STREET: 220 Montgomery Street, Suite 2200
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/011,366
/ FILING DATE: 16-Nov. US20030054493A1-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/957,310
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;; FILING DATE: 23-OCT-1997
;; APPLICATION NUMBER: US 08/329,154
;; FILING DATE: 24-OCT-1994
;; APPLICATION NUMBER: US 08/161,907
;; FILING DATE: 02-DEC-1993
;; APPLICATION NUMBER: US 07/985,321
;; FILING DATE: 04-DEC-1992
;; APPLICATION NUMBER: US 07/429,791
;; FILING DATE: 31-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: OPHD-01121
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match 63.2%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
Db 1 GCTCTAGATGA 12

RESULT 12
US-09-969-373-1959
; Sequence 1959, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1959
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1959

Query Match 57.9%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGG 19
Db 6 ATGAACGGTGG 16

RESULT 13
US-09-997-868-13/c
; Sequence 13, Application US/09997868
; Publication No. US20030031654A1
; GENERAL INFORMATION:

;; APPLICANT: Gorman, Cornelia M.,
;; Groskreutz, Debyra J.
;; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
;; Polypeptide Synthesis
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA: US/09/997,868
;; APPLICATION NUMBER: 07/887265
;; FILING DATE: 22-MAY-1992
;; APPLICATION NUMBER: 07/803631
;; FILING DATE: 06-DEC-1992
;; APPLICATION NUMBER: PCT/US92/10621
;; FILING DATE: 04-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P0748P3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match 57.9%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 11

RESULT 14
US-09-765-873A-5
; Sequence 5, Application US/09765873A
; Patent No. US20010053847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: primer

US-09-765-873A-5

Query Match 57.9% Score 11; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
| | | | | | | | | |
Db 3 GCTCTAGATG 13

RESULT 15

US-09-952-522B-9
; Sequence 9, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lluall, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: osteocalcin forward primer
US-09-952-522B-9

Query Match 57.9% Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
| | | | | | | | | |
Db 1 GCTCTAGATG 11

Search completed: June 23, 2003, 20:01:32
Job time : 152.681 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 29.749 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	2	US-08-770-565-9
2	19	100.0	26	1	US-08-330-123A-23
3	19	100.0	26	1	US-08-482-115B-23
4	19	100.0	26	2	US-08-660-678A-23
5	19	100.0	26	2	US-08-710-249-26
6	19	100.0	26	2	US-08-485-778-19
7	19	100.0	26	2	US-08-472-802C-24
8	19	100.0	26	3	US-08-520-550A-19
9	19	100.0	26	3	US-08-598-443-23
10	19	100.0	26	4	US-08-574-549A-598
11	19	100.0	26	4	US-09-060-523-23
12	19	100.0	26	4	US-09-220-157A-26
13	19	100.0	26	4	US-09-286-959B-4
14	19	100.0	26	4	US-09-580-517-23
15	19	100.0	27	4	US-08-770-565-26
16	19	100.0	30	2	US-08-770-565-8
17	18	94.7	30	2	US-08-770-565-6
18	15	78.9	15	2	US-08-770-565-10
19	14	73.7	27	3	US-08-770-565-17
20	14	73.7	27	4	US-09-375-419-24
21	13	68.4	18	4	US-08-974-549A-543
22	12	63.2	26	1	US-08-480-604A-16
23	12	63.2	26	2	US-08-405-496A-16
24	12	63.2	26	4	US-08-915-136-16
25	12	63.2	26	4	US-08-957-310-16
26	12	63.2	30	1	US-08-349-006-3
27	12	63.2	30	5	PCT-US94-02107-3

28	12	63.2	33	3	US-08-630-172-22	Sequence 22, Appl
29	12	63.2	33	4	US-09-375-419-22	Sequence 22, Appl
30	11	57.9	11	2	US-08-770-565-11	Sequence 11, Appl
31	11	57.9	21	4	US-08-026-143B-13	Sequence 13, Appl
32	11	57.9	21	5	PCT-US92-10621-13	Sequence 13, Appl
33	11	57.9	21	5	PCT-US94-02233-13	Sequence 13, Appl
34	11	57.9	22	4	US-09-627-216A-5	Sequence 5, Appl
35	11	57.9	23	3	US-08-973-068-46	Sequence 46, Appl
36	11	57.9	26	4	US-09-153-310-4	Sequence 4, Appl
37	11	57.9	30	2	US-08-995-927-7	Sequence 7, Appl
38	11	57.9	30	4	US-09-349-627-5	Sequence 5, Appl
39	11	57.9	30	4	US-09-582-096-7	Sequence 7, Appl
40	11	57.9	37	1	US-08-591-492-17	Sequence 17, Appl
41	11	57.9	37	3	US-08-815-190A-3	Sequence 3, Appl
42	11	57.9	39	4	US-09-091-305-3	Sequence 3, Appl
43	11	57.9	40	1	US-08-395-800A-12	Sequence 12, Appl
44	11	57.9	46	1	US-08-399-696-14	Sequence 14, Appl
45	11	57.9	50	1	US-08-374-641-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

Db 1 GCTCTAGATGAACGGTGG 19
|||||

RESULT 2
US-08-330-123A-23

; Sequence 23, Application US/08330123A
; Patent No. 5583016

; GENERAL INFORMATION:

; APPLICANT: VILLEPONTEAU, Bryant

; APPLICANT: FENG, Junli

; APPLICANT: FUNK, Walter

; APPLICANT: ANDREWS, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/330,123A

; FILING DATE: 27-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/272,102

; FILING DATE: 07-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15389-000810

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-330-123A-23

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 3

US-08-482-115B-23

; Sequence 23, Application US/08482115B

; Patent No. 5776679

; GENERAL INFORMATION:

; APPLICANT: VILLEPONTEAU, Bryant

; APPLICANT: FENG, Junli

; APPLICANT: FUNK, Walter

; APPLICANT: ANDREWS, William H.

; TITLE OF INVENTION: Assays for the RNA Component of Human

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/482,115B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/272,102

; FILING DATE: 07-JUL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/330,123

; FILING DATE: 27-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-000830US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-482-115B-23

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 4

US-08-660-678A-23

; Sequence 23, Application US/08660678A

; Patent No. 5837857

; GENERAL INFORMATION:

; APPLICANT: VILLEPONTEAU, Bryant

; APPLICANT: FENG, Junli

; APPLICANT: FUNK, Walter

; APPLICANT: ANDREWS, William H.

; TITLE OF INVENTION: Mammalian Telomerase

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,678A

; FILING DATE: 05-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 5
US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 6
US-08-485-778-19
Sequence 19, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05M4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 7
US-08-472-802C-24
; Sequence 24, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 8
US-08-520-550A-19
; Sequence 19, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-520-550A-19

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 9
US-08-998-443-23
; Sequence 23, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US/08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-09-220-157A-26
; Sequence 26, Application US/09220157A
; Patent No. 6300110
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 13
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 14
US-09-580-517-23
; Sequence 23, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; FUNK, Junli
;

```

ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
DB 5 GCTCTAGAAATGAACGGTGG 23

RESULT 15
US-08-770-565-26
Sequence 26, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0023000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-26

Query Match 100.0%; Score 19; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
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DB 5 GCTCTAGAAATGAACGGTGG 23

Search completed: June 23, 2003, 10:17:07
Job time : 30.749 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 126.263 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGACGGTGG 19

Scoring table: OLIGO NUC.

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.1*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	AAV41176	RNA component of h
2	19	100.0	25	AAZ08704	Human telomerase R
3	19	100.0	26	AAT10304	RNA component of h
4	19	100.0	26	AAT10299	RNA component of h
5	19	100.0	26	AAT11044	Primer for product
6	19	100.0	26	AAT58811	Human telomerase P
7	19	100.0	26	AAV19489	Human htr gene R
8	19	100.0	26	AAV17033	Telomerase PCR pri
9	19	100.0	26	AAZ90788	Human telomerase R

10	19	100.0	26	20	AAZ77402	Human telomerase R
11	19	100.0	26	20	AAZ01542	PCR primer for Hum
12	19	100.0	26	21	AAA88250	Human telomerase R
13	19	100.0	26	24	ABK48024	Human telomerase-a
14	19	100.0	26	24	ABK24246	Human telomerase (
15	19	100.0	27	19	AAV41193	RNA component of h
16	19	100.0	27	24	ABA95497	Human telomerase R
17	19	100.0	30	19	AAV63649	Antisense oligonuc
18	19	100.0	30	19	AAV41175	RNA component of h
19	19	100.0	30	20	AAZ23631	Human clone 28-1 t
20	19	100.0	30	22	AAZ09476	Antisense oligonuc
21	19	100.0	30	23	AAZ15928	Human telomerase p
22	19	100.0	30	24	ABA91517	Oligonucleotide us
23	15	78.9	15	19	AAV41177	RNA component of h
24	14	73.7	15	23	AAZ15931	Human telomerase p
25	14	73.7	27	18	AAT97049	Sense primer for h
26	13	68.4	13	23	AAZ15930	Human telomerase p
27	13	68.4	28	24	ABA04366	CRT C-domain-green
28	13	68.4	32	21	AAA46113	Human GPCR TDAG8(I
29	12	63.2	17	22	AAF57369	Murine Cdc25A intr
30	12	63.2	26	17	AAT29258	C. difficile toxin
31	12	63.2	26	19	AAZ30567	Clostridium diffic
32	12	63.2	26	21	ABK09963	Novel recombinant
33	12	63.2	30	15	AAQ71630	HCWV IR-exon-4 sub
34	12	63.2	33	18	AAT97047	Sense primer for h
35	12	63.2	39	22	AAF81502	Novel human G prot
36	12	63.2	39	22	AAF87602	DNA associated wit
37	11	57.9	11	19	AAV41178	RNA component of h
38	11	57.9	11	23	AAZ15929	Human telomerase p
39	11	57.9	15	23	AAZ15932	Human telomerase p
40	11	57.9	19	22	AAH43421	ISA3 reverse prime
41	11	57.9	21	14	AAQ43258	Sequence encoding
42	11	57.9	21	14	AAQ43257	Sequence encoding
43	11	57.9	21	15	AAQ71457	Rx 2-4 prorelaxin
44	11	57.9	22	24	AAZ33073	Phenylalanine ammo
45	11	57.9	22	24	AAZ26921	Rhodospiridium tor

ALIGNMENTS

RESULT 1
AAV41176
ID AAV41176 standard; DNA; 19 BP.
XX
AC AAV41176;
XX

DT 08-OCT-1998 (first entry)

XX RNA component of human telomerase (htr) antisense oligo 21ab.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; htr;
KW immune system down-regulation; anti-inflammatory therapy; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

XX 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

XX 20-DEC-1996; 96US-0770564.

PA (GERO-) GERON CORP.

XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

XX New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AA41169 to AA41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilization, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence: 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 19; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
Db 1 GCTCTAGATGAACGGTGG 19
RESULT 2
AAZ08704
ID AAZ08704 standard; DNA; 25 BP.
XX
AC AAZ08704;
XX
DT 20-OCT-1999 (first entry)
XX
DE Human telomerase RNA template PCR primer R3C.
XX
KW Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
KW telomeric repeat amplification protocol; detection; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9941406-A1.
XX
PD 19-AUG-1999.
XX
XX 16-FEB-1999; 99WO-US03302.
PF 16-FEB-1998; 98US-0074793.
PR
XX (UTMA-) UNIV MARYLAND BALTIMORE.
PA
XX Abruzzo LV, Highsmith E, Stamberg J, Strovel JW;
XX WPI; 1999-508655/42.
XX
XX Detecting telomerase activity in non-cellular body fluid using a
PT modified telomeric repeat amplification protocol
XX

PS Disclosure; Page 16; 32pp; English.
XX
XX A method has been developed for detecting telomerase activity in a
CC non-cellular portion of body fluid from a cancer patient using a
CC modified telomeric repeat amplification protocol (TRAP). A method for
CC detecting cancer comprises: (a) removing the cellular portion of a body
CC fluid specimen from the patient; (b) preparing a protein extract from
CC the body fluid remainder; (c) assaying the extract for the presence and
CC quantity of telomerase RNA or telomerase activity; and (d) comparing the
CC results with normal levels, to determine the presence of cancer. The
CC methods are used in cancer diagnosis and prognosis, and also to monitor
CC cancer therapy effectiveness. Unlike prior art telomerase activity
CC assays in cancer patients, the method allows noninvasive sample
CC collection. The methods are also more reliable and less tumour specific
CC than other methods which detect circulating tumour markers. The present
CC sequence represents a human telomerase RNA template PCR primer used in
CC the exemplification of the present invention.
XX
SQ Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
Query Match 100.0%; Score 19; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
Db 4 GCTCTAGATGAACGGTGG 22
RESULT 3
AAT10304
ID AAT10304 standard; DNA; 26 BP.
XX
AC AAT10304;
XX
DT 10-SEP-1996 (first entry)
XX
DE RNA component of human telomerase nested PCR primer R3c.
XX
KW RNA component; human; telomerase; polymerase chain reaction;
KW recombinant production; synthesis; mutant; detection; mammalian;
KW identification; modulating agent; neoplastic condition;
KW transcriptional regulatory sequence; gene therapy; disease;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9601835-A1.
XX
PD 25-JAN-1996.
XX
XX 06-JUL-1995; 95WO-US08530.
PF
XX 07-JUN-1995; 95US-0482115.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 07-JUN-1995; 95US-0472802.
XX
XX (GERO-) GERON CORP.
PA
XX Andrews WH, Feng J, Funk W, Villeponteau B;
PI WPI; 1996-097581/10.
XX
XX RNA component of mammalian telomerase, esp. human - useful in
PT identifying e.g. candidate telomerase-modulating agents
XX
XX Example 10; Page 82; 114pp; English.
XX
XX The present sequence, a nested PCR primer for the RNA component
CC of human telomerase (RCHT), was used in a 5' RACE procedure. The
CC RCHT can be used in the recombinant prodn. of an active telomerase
CC mol., capable of adding sequences to chromosomal DNA telomeres, and

CC in the synthesis of mutant sequences for the detection of mutant
 CC mammalian telomerase RNA component polynucleotides. The RCHT may
 CC also be used in the identification of telomerase modulating agents,
 CC and in the detection of telomerase related, or neoplastic
 CC conditions in a patient. Polynucleotides of at least 25
 CC consecutive nucleotides identical, or complementary to the RCHT
 CC sequence linked to heterologous transcriptional regulatory
 CC sequences, can be used for the gene therapy of human diseases.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041; 0; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 4

AAT10299

ID AAT10299 standard; DNA; 26 BP.

XX AC AAT10299;

XX DT 09-SEP-1996 (first entry)

XX RNA component of human telomerase antisense plasmid PCR primer R3C.

XX RNA component; human; telomerase; lung fibroblast; cell line WI-38;
 KW recombinant production; synthesis; mutant; detection; mammalian;
 KW identification; modulating agent; neoplastic condition;
 KW transcriptional regulatory sequence; gene therapy; disease;
 KW polymerase chain reaction; antisense plasmid; PCR primer; ss.

XX Synthetic.

XX WO9601835-A1.

XX 25-JAN-1996.

XX 06-JUL-1995; 95WO-US08530.

XX 07-JUN-1995; 95US-0482115.

XX 07-JUL-1994; 94US-0272102.

XX 27-OCT-1994; 94US-0330123.

XX 07-JUN-1995; 95US-0472802.

XX (GERO-) GERON CORP.

XX Andrews WH, Feng J, Funk W, Villeponteau B;

XX WPI; 1996-097581/10.

XX RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents

XX Example 8; Page 80; 114pp; English.

XX The present sequence is a PCR primer for a RNA component of human
 CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
 CC genomic DNA library obtd. from the human lung fibroblast cell line
 CC WI-38. The RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene

CC therapy of human diseases.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041; 0; Mismatches 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 5

AAT11044

ID AAT11044 standard; DNA; 26 BP.

XX AC AAT11044;

XX DT 02-JUL-1996 (first entry)

XX Primer for production of telomerase antisense oligonucleotide.
 DE Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.

XX Synthetic.

XX WO9601614-A2.

XX 25-JAN-1996.

XX 07-JUL-1995; 95WO-US08620.

XX 07-JUN-1995; 95US-0485778.

XX 07-JUL-1994; 94US-0272102.

XX 27-OCT-1994; 94US-0330123.

XX 13-FEB-1995; 95US-0387524.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (GERO-) GERON CORP.

XX Andrews WH, Avillon AA, Feng J, Funk W, Greider C;

XX Marhuenda NA, Villeponteau B;

XX WPI; 1996-097428/10.

XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation

XX Example 8; Page 53; 85pp; English.

XX The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation.
 CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
 CC antisense oligonucleotides which were then used to produce antisense
 CC expression plasmids. AAT11040 was used alongside both AAT11043 and
 CC AAT11044 to produce two different antisense molecules.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041; 0; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 DB 5 GCTCTAGATGAACGGTGG 23

RESULT 6

AAAT58811
 ID AAT58811 standard; DNA; 26 BP.
 AC AAT58811;
 XX
 XX
 DT 20-NOV-1997 (first entry)
 XX
 XX Human telomerase PCR 3'-primer R3C.

XX Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.
 XX
 XX Synthetic.

OS WO9640868-A1.

PN 19-DEC-1996.

PD 06-JUN-1996; 96WO-US09517.

PF 07-JUN-1995; 95US-0478352.

PR (COLD-) COLD SPRING HARBOR LAB.

XX Autexier C, Greider C;

XX WPI; 1997-099928/09.

XX DNA encoding essential RNA components of human telomerase - also

XX truncated or recombinant telomerase, useful for diagnosis and

XX treatment of cancer and infection by eukaryotic parasites

XX Example 5; Page 32; 48pp; English.

XX The present sequence represents PCR 3'-primer R3C used for

XX amplifying the human telomerase (hTR). The RNA and DNA can be used in

XX hybridisation assays to detect or quantify telomerase activity in cells,

XX tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites

XX (yeast and protozoa) or tumours. It is also useful as primers for

XX amplification assays. The truncated or recombinant vertebrate telomerase

XX is used therapeutically to increase telomerase activity (also as

XX reagents in the screening assay) while the RNA or other inhibitors such

XX as antisense molecules, are used to reduce such activity. Typical

XX applications are initiation/restoration of activity to cause senescence

XX or to prevent immortalisation of cells in tumours or parasites. The DNA

XX is also used to produce recombinant telomerase, which can then be used

XX conventionally to raise antibodies for diagnostic detection of

XX telomerase. Detecting telomerase allows early diagnosis of tumour or

XX infection, before clinical signs manifest. Telomerase inhibitors

XX directed against e.g. Trypanosoma should cause fewer side effects than

XX drugs currently used to treat such infections. The DNA encodes those

XX parts of hTR RNA essential for activity but are significantly shorter

XX than the endogenous RNA component.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

XX Query Match 100.0%; Score 19; DB 18; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.041;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 DB 5 GCTCTAGATGAACGGTGG 23

RESULT 7

AAAT58811
 ID AAT58811 standard; DNA; 26 BP.
 AC AAT58811;
 XX
 XX
 DT 20-NOV-1997 (first entry)
 XX
 XX Human telomerase PCR 3'-primer R3C.

XX Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.
 XX
 XX Synthetic.

OS WO9640868-A1.

PN 19-DEC-1996.

PD 06-JUN-1996; 96WO-US09517.

PF 07-JUN-1995; 95US-0478352.

PR (COLD-) COLD SPRING HARBOR LAB.

XX Autexier C, Greider C;

XX WPI; 1997-099928/09.

XX DNA encoding essential RNA components of human telomerase - also

XX truncated or recombinant telomerase, useful for diagnosis and

XX treatment of cancer and infection by eukaryotic parasites

XX Example 5; Page 32; 48pp; English.

XX The present sequence represents PCR 3'-primer R3C used for

XX amplifying the human telomerase (hTR). The RNA and DNA can be used in

XX hybridisation assays to detect or quantify telomerase activity in cells,

XX tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites

XX (yeast and protozoa) or tumours. It is also useful as primers for

XX amplification assays. The truncated or recombinant vertebrate telomerase

XX is used therapeutically to increase telomerase activity (also as

XX reagents in the screening assay) while the RNA or other inhibitors such

XX as antisense molecules, are used to reduce such activity. Typical

XX applications are initiation/restoration of activity to cause senescence

XX or to prevent immortalisation of cells in tumours or parasites. The DNA

XX is also used to produce recombinant telomerase, which can then be used

XX conventionally to raise antibodies for diagnostic detection of

XX telomerase. Detecting telomerase allows early diagnosis of tumour or

XX infection, before clinical signs manifest. Telomerase inhibitors

XX directed against e.g. Trypanosoma should cause fewer side effects than

XX drugs currently used to treat such infections. The DNA encodes those

XX parts of hTR RNA essential for activity but are significantly shorter

XX than the endogenous RNA component.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

XX Query Match 100.0%; Score 19; DB 18; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.041;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAV19489 standard; DNA; 26 BP.
 AC AAV19489;
 XX
 XX
 DT 28-AUG-1998 (first entry)
 XX
 XX Human hTR gene RT-PCR primer R3c.

XX hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;

XX gene therapy; diagnosis; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9811204-A1.

XX 19-WAR-1998.

XX 13-SEP-1996; 96WO-US14679.

XX 13-SEP-1996; 96WO-US14679.

XX (GERO-) GERON CORP.

XX Adams RR, Andrews WH, Feng J, Villeponteau B;

XX WPI; 1998-207373/18.

XX Human TPC2, TPC3 and TR genes - regulate telomere length or modulate

XX telomerase activity

XX Disclosure; Page 49; 86pp; English.

XX Primers R3c and R3b (see AAV19488) were designed for the PCR

XX amplification of the human telomerase hTR gene (see AAV19481). hTR

XX mRNA levels were showed to correlate with telomerase activity

XX levels in a variety of mortal and immortal cell lines. Methods of

XX the invention allow detection and quantitation of TPC2 (see

XX AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be

XX used to detect immortal cells, especially telomerase positive

XX cancer cells.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

XX Query Match 100.0%; Score 19; DB 19; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.041;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 8

AAV17033

ID AAV17033 standard; DNA; 26 BP.

AC AAV17033;

XX 13-AUG-1998 (first entry)

XX Telomerase PCR primer R3c.

XX Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;

XX prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;

XX PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.
 XX 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX Example 2; Page 218; 387pp; English.
 XX The present sequence represents a PCR primer from the present invention
 CC which describes human telomerase reverse transcriptase (hTERT). The
 CC present invention also describes the following methods: (A) determining
 CC whether a test compound is a modulator of hTERT, by detecting the change
 CC in hTERT recombinant protein or polynucleotide, on administration of the
 CC compound; (B) preparation of recombinant telomerase by contacting a
 CC protein preparation of hTERT with a telomerase RNA component; (C)
 CC detection of the hTERT RNA or protein in a sample by binding a relevant
 CC probe to the sample and detecting the complex formed or in the case of
 CC RNA detection, amplifying the product and correlating the presence of
 CC complex or amplification product with presence of hTERT in the sample;
 CC and (D) increasing the proliferation of a vertebrate cell by increasing
 CC hTERT expression; and (E) the use of an agent that causes an increase in
 CC cell vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 19; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGG 19
 Db 5 GCTCTAGATGAACGGTGG 23
 RESULT 9
 AAX90788
 ID AAX90788 standard; DNA; 26 BP.
 XX AAX90788;
 AC AAX90788;
 XX 13-JAN-2000 (first entry)
 DT Human telomerase RNA specific PCR primer-2.
 XX PCR primer; human telomerase RNA; hTR; amplify; human staufen cDNA;
 KW hStau; synthesised; random hexamer primer;
 KW Superscript II reverse transcriptase; ss.
 XX Synthetic.

OS Homo sapiens.
 XX WO9951255-A1.
 PN 14-OCT-1999.
 PD 06-APR-1999; 99WO-US07533.
 PF 06-APR-1998; 98US-0080783.
 PR (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA Greider CW, Le S;
 PI WPI; 1999-620168/53.
 DR Human staufen polypeptide useful in methods for identifying telomerase
 PT inhibitors -
 PT Disclosure; Page 15; 50pp; English.
 PS The present sequence is a PCR primer specific to human telomerase
 CC RNA (hTR). It is used to amplify human staufen (hStau) cDNA synthesised
 CC using random hexamer primers and Superscript II reverse transcriptase.
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 19; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGG 19
 Db 5 GCTCTAGATGAACGGTGG 23
 RESULT 10
 AAX77402
 ID AAX77402 standard; DNA; 26 BP.
 XX AAX77402;
 AC AAX77402;
 XX 05-AUG-1999 (first entry)
 DT Human telomerase RNA PCR primer TB-hTR3.1.
 DE Telomerase; human; diagnosis; bladder cancer; detection; urine;
 XX PCR primer; ss.
 KW Synthetic.
 XX Homo sapiens.
 XX EP926245-A2.
 PN 30-JUN-1999.
 PD 21-DEC-1998; 98EP-0124326.
 PF 22-DEC-1997; 97DE-1057300.
 PR (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX Emrich T;
 PI WPI; 1999-349242/30.
 DR Detecting telomerase RNA in urine - useful for diagnosis of bladder
 XX cancer
 PT Claim 6; Page 10; 13pp; German.
 PS This invention describes a novel method for diagnosing bladder cancer
 XX which comprises detecting telomerase RNA in a urine sample. The method
 CC

CC of the invention has greater sensitivity and reliability than assays for
 CC telomerase activity (cf. WO 9735871). This sequence represents a primer
 CC used in the method of the invention.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 11

AAK01542

ID AAX01542 standard; DNA; 26 BP.

XX AC

XX AAX01542;

XX 29-APR-1999 (first entry)

XX DE

XX PCR primer for Human TPC3 gene.

XX TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;

XX fertility; diagnosis; therapy; PCR primer; ss.

XX OS

XX Synthetic.

XX OS Homo sapiens.

XX PN

XX US5858777-A.

XX PD

XX 12-JAN-1999.

XX PF

XX 13-SEP-1996; 96US-0710249.

XX PR

XX 08-SEP-1995; 95US-0003492.

XX PR

XX 05-JAN-1996; 96US-0583808.

XX PR

XX 13-SEP-1996; 96US-0710249.

XX PA

XX (GERO-) GERON CORP.

XX PI

XX Adams RR, Andrews WH, Feng J, Villeponteau B;

XX DR

XX WPI; 1999-152104/13.

XX PT

XX DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere

XX length or modulating telomerase activity

XX PS

XX Example; Column 38; 59pp; English.

XX CC

CC This sequence represents a PCR primer for DNA encoding the human TPC3
 CC protein, which is contained within the recombinant mammalian host cell of
 CC the invention. The invention provides methods and reagents for regulating
 CC telomere length and modulating telomerase activity in mammalian cells as
 CC well as for detecting, diagnosing, and treating related diseases and
 CC conditions such as cancer, pregnancy, or fertility in humans and other
 CC mammals.

XX SQ

Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 12

AAA88250

ID AAA88250 standard; DNA; 26 BP.

XX AC

XX AAA88250;

XX DT

XX 15-DEC-2000 (first entry)

XX DE

XX Human telomerase RNA reverse transcriptase PCR primer #2.

XX KW

XX Human; telomerase; hTR; reverse transcriptase; RT-PCR; PCR primer;

XX KW

XX detection; cancer; micrometastasis; diagnosis; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200046601-A1.

XX PD

XX 10-AUG-2000.

XX PF

XX 01-FEB-2000; 2000WO-IB00100.

XX PR

XX 02-FEB-1999; 99GB-0002302.

XX PA

XX (LABS/) LARSEN F.

XX PA

XX (SKAA/) SKAANSENG M.

XX PI

XX Larsen F, Skaanseng M;

XX DR

XX WPI; 2000-491281/43.

XX PT

XX Detecting telomerase activity in samples, useful for diagnosis of
 XX cancer and micrometastasis, comprises treating sample with solid phase,
 XX removing solid phase and treating to elute bound telomerase

XX PS

XX Example 11; Page 38; 68pp; English.

XX CC

CC The present invention describes a method (I) for detecting telomerase
 CC activity in a sample. The method comprises treating the sample with a
 CC solid phase to bind telomerase, separating the solid phase from the
 CC sample to form a test sample which may be treated to elute bound
 CC telomerase and assaying the sample for telomerase activity. Also
 CC described are: (i) a kit (ii) for detecting telomerase activity,
 CC comprising a solid phase and one or more components for assaying
 CC telomerase activity; and (2) a component (iii) of an assay system for
 CC detecting telomerase activity, comprising a solid phase for binding
 CC telomerase on which is present a substrate for telomerase elongation.
 CC (i) is useful for cancer diagnosis or prognosis and detection of
 CC micrometastasis as detection of telomerase activity is indicative of
 CC cancer or micrometastasis. The solid phase used in (i) is useful for
 CC separating telomerase from a sample and therefore for detecting
 CC telomerase activity. (ii) is useful for detection of cancer cells and
 CC may also comprise means for assaying an mRNA diagnostic for cancer.
 CC The present sequence represents a reverse transcriptase (RT) PCR primer
 CC for human telomerase RNA, which is used in an example from the present
 CC invention.

XX SQ

Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

DB 5 GCTCTAGATGAACGGTGG 23

RESULT 13

ABK48024

ID ABK48024 standard; DNA; 26 BP.

XX AC

XX ABK48024;

XX DT

XX 18-JUN-2002 (first entry)

XX XX

DE Human telomerase-associated RNA template (hTR), PCR primer hTR2.
XX Human; telomerase-associated RNA template; hTR; endometrial;
KW malignancy; cancer; breast; ovarian; head and neck; lung; cervical;
KW colorectal; gastric; liver; pancreatic; bladder; prostate;
KW brain; kidney; oesophagus; melanoma; sarcoma; premalignancy;
KW carcinoma in-situ; cervical dysplasia; bronchial dysplasia;
KW cervical intraepithelial neoplasia; atypical hyperplasia;
KW colorectal adenoma; atypical endometrial hyperplasia; tumour;
KW Barrett's oesophagus; telomerase-directed therapy; primer; ss.
XX Homo sapiens.
OS
XX
XX WO200218652-A2.
PN
XX
XX PD 07-MAR-2002.
PD
XX PF 28-AUG-2001; 2001WO-US26749.
PF
XX PR 31-AUG-2000; 2000US-0653573.
PR
XX (ONCO-) ONCOMEDX INC.
XX
XX PA Koperski MS, Gocke CD;
PA
XX PI
XX PS WPI; 2002-269532/31.
PS
XX PT Detecting human telomerase RNA template RNA or human telomerase reverse
PT transcriptase protein RNA in bodily fluid, useful as marker for
PT diagnosing, monitoring or treating cancer, carcinoma in situ or
PT premalignancy -
XX
XX Example 1; Page 14; 30pp; English.
XX
XX The invention relates to detecting human telomerase RNA template (hTR)
CC RNA or human telomerase reverse transcriptase protein RNA (hTRT) RNA (I)
CC in a bodily fluid, comprising amplifying RNA extracted from plasma or
CC serum sample, or its corresponding cDNA comprising (I), using primers or
CC probes that target (I) or cDNA and detecting qualitatively or
CC quantitatively amplified product of (I) or cDNA product. The method is
CC useful for detecting (I) in a bodily fluid, which is useful for
CC identifying a human having (I) expressing cells or tissue which
CC include a malignancy preferably a cancer of breast, ovarian, head and
CC neck, lung, cervical, colorectal, gastric, liver, pancreatic, bladder,
CC prostate, endometrial, brain, kidney, or oesophagus, or a melanoma or
CC sarcoma, premalignancy or carcinoma in-situ, preferably cervical
CC dysplasia, cervical intraepithelial neoplasia, bronchial dysplasia,
CC atypical hyperplasia of the breast, ductal carcinoma in-situ,
CC colorectal adenoma, atypical endometrial hyperplasia, or Barrett's
CC oesophagus, where the human is at risk for developing a malignancy or
CC premalignancy or is known to have malignancy, premalignancy or
CC carcinoma in situ. The method is also useful for treating a human with
CC cancer for telomerase-directed therapy, which comprises selecting the
CC human for the therapy after detection of (I), for determining a
CC need for diagnostic test in a human with malignancy or premalignancy
CC and for monitoring a therapy administered to a human. (I) provides a
CC marker which is utilised as a guide to whether adequate therapeutic
CC effect has been achieved, or whether additional or more advanced therapy
CC is required, and to assess prognosis in these patients. The method also
CC allows identification or analysis, either quantitatively or
CC qualitatively, of (I) in plasma or serum of humans during or following
CC surgical procedures to remove premalignant or malignant lesions, and thus
CC allow stratification of such patients as to their risk of residual
CC cancer following surgery, and their need for further therapy or who has
CC completed therapy as an early indicator or relapsed cancer, impending
CC relapse, or treatment failure. The method allows the development and
CC application of telomerase-specific therapy even when only premalignant
CC tumours, early cancer, or occult cancer or metastasis such as following
CC resection or in minimal residual disease are present. The present
CC sequence represents a PCR primer for human telomerase-associated
CC RNA template (hTR).
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23
|||||
RESULT 14
AAD24246
ID AAD24246 standard; DNA; 26 BP.
XX
XX AC AAD24246;
XX
XX DT 07-MAR-2002 (first entry)
XX
XX DE Human telomerase (hTR) cDNA amplifying R3c downstream RT-PCR primer.
XX
XX KW Human; telomerase; TR; telomerase activity-related disease; therapy;
KW cancer; pregnancy; fertility; RT-PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN US6300110-B1.
XX
XX PD 09-OCT-2001.
XX
XX PF 23-DEC-1998; 98US-0220157.
XX
XX PR 09-SEP-1995; 95US-003492P.
PR 13-SEP-1996; 96US-0710249.
PR 05-JAN-1996; 96US-0583808.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Villeponteau B, Feng J, Andrews WH, Adams RR;
XX WPI; 2002-033174/04.
XX
XX PT Peptide products of the human TPC2 and TPC3 gene are involved in
PT regulation of telomere length and activity are useful to diagnose and
PT treat telomere length and activity-related diseases -
XX
XX PS Example; Column 38; 60pp; English.
XX
XX CC The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is a reverse transcription (RT) PCR primer
CC used for amplifying human telomerase (hTR) cDNA.
XX
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
Query Match 100.0%; Score 19; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23
|||||
RESULT 15
AAV41193
ID AAV41193 standard; DNA; 27 BP.
XX

AC AAV41193;
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE RNA component of human telomerase (hTR) amplifying reverse primer.
 XX
 DE RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; RT-PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9828442-A1.
 XX
 PD 02-JUL-1998.
 XX
 PF 19-DEC-1997; 97WO-US23619.
 XX
 PR 20-DEC-1996; 96US-0770565.
 PR 20-DEC-1996; 96US-0770564.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
 XX
 DR WPI; 1998-377670/32.
 XX
 PT New polynucleotide(s) anti:sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 65; Page 75; 80pp; English.
 XX
 CC This primer is used for the RT-PCR amplification of an RNA component of
 CC human telomerase (hTR). This is used in the method of invention of
 CC determining the amount of hTR in a sample. The method comprises
 CC amplifying a sequence of hTR and a control polynucleotide from a sample
 CC and determining an amount of amplified hTR and an amount of amplified
 CC control polynucleotide. The amount of amplified hTR is normalised with
 CC respect to the amount of amplified control polynucleotide to provide a
 CC normalised amount of hTR which provides a determination of the amount of
 CC hTR in the sample. The invention provides antisense oligonucleotides to
 CC the hTR which may specifically be used for detection of an RNA component
 CC of human telomerase in a sample. This is useful for diagnosing cancer
 CC (especially neuroblastoma, bladder, colon and prostate cancer), and
 CC providing prognosis for a cancer patient. The antisense oligonucleotides
 CC can be used for inhibiting telomerase activity in both cultured cells and
 CC in cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in anti-
 CC inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 5 GCTCTAGATGAACGGTGG 23
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Search completed: June 23, 2003, 05:43:38
 Job time : 126.571 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 220.96 Seconds
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Title: US-08-770-564A-9
 Perfect score: 19
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Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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1	19	100.0	19	6	AR063833 Sequence
2	19	100.0	26	6	A94988 Sequence 2
3	19	100.0	26	6	AR016055 Sequence
4	19	100.0	26	6	AR028786 Sequence
5	19	100.0	26	6	AR059216 Sequence
6	19	100.0	26	6	AR075527 Sequence
7	19	100.0	26	6	AR161925 Sequence
8	19	100.0	26	6	AX022187 Sequence
9	19	100.0	26	6	AX033377 Sequence
10	19	100.0	26	6	AX468455 Sequence
11	19	100.0	26	6	BD011297 Human tel
12	19	100.0	26	6	E36508 Method for
13	19	100.0	26	6	E37046 Human telom
14	19	100.0	26	6	I31770 Sequence 23
15	19	100.0	27	6	AR063850 Sequence
16	19	100.0	27	6	AX117989 Sequence
17	19	100.0	30	6	AR063832 Sequence
18	19	100.0	30	6	AX465471 Sequence
19	18	94.7	30	6	A84596 Sequence 6
20	18	94.7	30	6	AR079893 Sequence
21	15	78.9	15	6	AR063834 Sequence
22	13	68.4	18	6	BD011244 Human tel
23	13	68.4	18	6	E36993 Human telom
24	13	68.4	28	6	AX298137 Sequence
25	12	63.2	17	6	AX099957 Sequence
26	12	63.2	15	6	I04124 Sequence 8
27	12	63.2	26	6	AR000025 Sequence
28	12	63.2	26	6	AR169136 Sequence
29	12	63.2	26	6	AR202623 Sequence
30	12	63.2	26	6	AX036237 Sequence
31	12	63.2	30	6	I25474 Sequence 3
32	12	63.2	36	6	I04342 Sequence 6
33	12	63.2	39	6	E49124 Novel G pro
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35	11	57.9	11	6	AR063835 Sequence
36	11	57.9	19	6	AX244257 Sequence
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40	11	57.9	22	6	AX370655 Sequence
41	11	57.9	23	6	AR112025 Sequence
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45	11	57.9	26	6	AR179447 Sequence

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION
 AR063833
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AR063833
 Sequence 9 from patent US 5846723.
 AR063833.1 GI:5993141
 Unknown.
 Unclassified.
 1 (bases 1 to 19)
 Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
 Methods for detecting the RNA component of telomerase
 Patent: US 5846723-A 9 08-DEC-1998;
 Location/Qualifiers

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DEFINITION Sequence 2 from Patent EP0926245.
ACCESSION A94988
VERSION A94988.1 GI:6779168
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Methods and reagents for regulating telomere length and telomerase
JOURNAL activity: US 5858777-A 26 12-JAN-1999;
FEATURES Patent: US 5858777-A 26 12-JAN-1999;
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Db 5 GCTCTAGAAATGAACGGTGG 23

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DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES Location/Qualifiers
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DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methods and reagents for regulating telomere length and telomerase
JOURNAL activity: US 5858777-A 26 12-JAN-1999;
FEATURES Patent: US 5858777-A 26 12-JAN-1999;
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DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
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DEFINITION Sequence 24 from patent US 5958680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
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TITLE      Mammalian telomerase
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DEFINITION Sequence 23 from patent US 6258535.
ACCESSION  AR161925
VERSION     AR161925.1 GI:16228953
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SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 6258535-A 23 10-JUL-2001;
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LOCUS      AX022187          26 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent EP0953042.
ACCESSION  AX022187
VERSION     AX022187.1 GI:10045855
KEYWORDS   '
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Andrews,W.H., Villeponteau,B., Adams,R.R. and Peng,J.
TITLE     Methods and reagents for regulating telomere length and telomerase
          activity
JOURNAL   Patent: EP 0953042-A 26 03-NOV-1999;
          GERON CORP (US)
FEATURES   Location/Qualifiers
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TITLE      Mammalian telomerase
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Db 5 GCTCTAGATGAACGGTGG 23

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LOCUS      AX033377          26 bp      DNA      linear      PAT 21-SEP-2000
DEFINITION Sequence 9 from Patent WO0046601.
ACCESSION  AX033377
VERSION     AX033377.1 GI:10280151
KEYWORDS   '
SOURCE     synthetic construct.
ORGANISM   synthetic construct
          artificial sequences.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Larsen,P. and Skaaneeng,M.
TITLE     Detecting telomerase activity
JOURNAL   Patent: WO 0046601-A 9 10-AUG-2000;
          LARSEN FRANK (NO); SKAANESENG MARIANNE (NO)
FEATURES   Location/Qualifiers
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DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION  AX468455
VERSION     AX468455.1 GI:21901291
KEYWORDS   '
SOURCE     human.
ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Kopreski,M.S. and Gocke,C.D.
TITLE     Method for detection of htr and htert telomerase-associated rna in
          plasma or serum
JOURNAL   Patent: WO 0218652-A 5 07-MAR-2002;
          Oncomedx, Inc. (US)
FEATURES   Location/Qualifiers
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RESULT 11
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DEFINITION
ACCESSION  BD011297
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
BASE COUNT
ORIGIN
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DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011297
VERSION BD011297.1 GI:18639670
KEYWORDS JP 2001081042-A/254.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
        Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 254 27-MAR-2001;
        GERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 2001081042-A/254
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        PF 27-JUL-2000 JP 2000227474
        PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
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        09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
        14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
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LOCUS 26 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for detecting bladder cancer in urine samples.
ACCESSION E36508
VERSION E36508
KEYWORDS JP 1999243995-A/2.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Thomas,E.
TITLE Method for detecting bladder cancer in urine samples
JOURNAL Patent: JP 1999243995-A 2 14-SEP-1999;
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COMMENT OS Artificial Sequence
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        PD 14-SEP-1999
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        PI THOMAS ENRIHI

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LOCUS 26 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E37046
VERSION E37046.1 GI:130233009
KEYWORDS JP 1999253177-A/254.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
        Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 254 21-SEP-1999;
        JERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 1999253177-A/254
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        PF 15-OCT-1998 JP 1998320169
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        25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR
        09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR
        14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI THOMAS
        R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
        MORIN,
        PI CALVIN B HAREI,WILLIAM H ANDREWS
        PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
        PC C12Q1/02,
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        PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
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DEFINITION  Sequence 23 from patent US 5583016.
ACCESSION  I31770
VERSION    I31770.1 GI:1822561
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 5583016-A 23 10-DEC-1996;
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ACCESSION  AR063850
VERSION    AR063850.1 GI:5993158
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SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 27)
AUTHORS   Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE     Methods for detecting the RNA component of telomerase
JOURNAL   Patent: US 5846723-A 26 08-DEC-1998;
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GenCore version 5.1.6
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(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	100.0	21	1	PCT-US03-04088-539
C 2	15	100.0	21	1	PCT-US03-04088-543
C 3	15	100.0	21	1	PCT-US03-04088-547
C 4	15	100.0	21	1	PCT-US03-04088-551
C 5	15	100.0	21	1	PCT-US03-04088-555
C 6	15	100.0	21	1	PCT-US03-04088-559
C 7	15	100.0	23	1	PCT-US03-04088-520
C 8	15	100.0	23	1	PCT-US03-04088-521
C 9	15	100.0	26	6	US-09-721-456-598
C 10	15	100.0	26	9	US-10-325-810-598
C 11	15	100.0	26	9	US-10-359-935-23
C 12	15	100.0	30	10	US-10-330-872-5
C 13	15	100.0	30	10	US-10-330-872A-5
C 14	14	93.3	23	9	US-10-310-188-36216
C 15	14	93.3	25	12	US-60-427-808-952738
C 16	14	93.3	25	13	US-60-469-545-13722
C 17	14	93.3	25	13	US-60-469-545-222991
C 18	13.4	89.3	18	6	US-09-721-456-543
C 19	13.4	89.3	18	9	US-10-325-810-543
C 20	13.4	89.3	25	7	US-09-954-445A-54976

C 21	13.4	89.3	25	9	US-10-355-577-981444	Sequence 981444,
C 22	13.4	89.3	25	12	US-60-427-836-494214	Sequence 494214,
C 23	13	86.7	21	1	PCT-US03-04088-538	Sequence 538, App
C 24	13	86.7	21	1	PCT-US03-04088-542	Sequence 542, App
C 25	13	86.7	21	1	PCT-US03-04088-546	Sequence 546, App
C 26	13	86.7	21	1	PCT-US03-04088-550	Sequence 550, App
C 27	13	86.7	21	1	PCT-US03-04088-554	Sequence 554, App
C 28	13	86.7	21	1	PCT-US03-04088-558	Sequence 558, App
C 29	13	86.7	25	6	US-09-660-222-3845	Sequence 3845, App
C 30	13	86.7	25	6	US-09-660-222-3846	Sequence 3846, App
C 31	13	86.7	25	6	US-09-660-222-3854	Sequence 3854, App
C 32	13	86.7	25	9	US-10-098-263B-118949	Sequence 118949,
C 33	13	86.7	25	9	US-10-355-577-173196	Sequence 173196,
C 34	13	86.7	25	12	US-60-427-808-738286	Sequence 738286,
C 35	13	86.7	25	12	US-60-427-836-267834	Sequence 267834,
C 36	12.4	82.7	25	6	US-09-660-222-121265	Sequence 121265,
C 37	12.4	82.7	25	9	US-10-355-577-70333	Sequence 70333, A
C 38	12.4	82.7	25	9	US-10-355-577-482963	Sequence 482963,
C 39	12.4	82.7	25	9	US-10-355-577-704066	Sequence 704066,
C 40	12.4	82.7	25	9	US-10-355-577-751232	Sequence 751232,
C 41	12.4	82.7	25	9	US-10-355-577-956874	Sequence 956874,
C 42	12.4	82.7	25	12	US-60-427-808-51166	Sequence 51166, A
C 43	12.4	82.7	25	12	US-60-427-808-44453	Sequence 44453,
C 44	12.4	82.7	25	12	US-60-427-808-952737	Sequence 952737,
C 45	12.4	82.7	25	12	US-60-427-836-153966	Sequence 153966,

ALIGNMENTS

RESULT 1
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggan, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 15; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
    |||||
Db 19 GCTCTAGATGAACG 5

RESULT 2
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; FEATURE:
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxybasic moiety
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
    |||||
Db 1 GCUCUAGAUGAACG 15

RESULT 3
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
```

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; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; PCT-US03-04088-551

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. NO. 1.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCUCUAGAAUGAACG 15

RESULT 5
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

```

NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||:|||||
Db 19 GCTCTAGAAATGAACG 5

RESULT 6

PCT-US03-04088-559
Sequence 559, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 559
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
OTHER INFORMATION: antisense region

NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(5)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6)..(9)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)..(10)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature

LOCATION: (14)..(14)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||:|||||
Db 1 GCUCUAGAAUGAACG 15

RESULT 7

PCT-US03-04088-520/c
Sequence 520, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 520
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 100.0%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 23 GCTCTAGAAATGAACG 9

RESULT 8
 PCT-US03-04088-521/c
 ; Sequence 521, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 521
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-521

Query Match 100.0%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 21 GCTCTAGAAATGAACG 7

RESULT 9
 US-09-721-456-598
 ; Sequence 598, Application US/09721456
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco

Query Match 100.0%; Score 15; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 5 GCTCTAGAAATGAACG 19

RESULT 10
 US-10-325-810-598
 ; Sequence 598, Application US/10325810
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.

STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 598:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..26
 OTHER INFORMATION: /note= "R3c primer"
 SEQUENCE DESCRIPTION: SEQ ID NO: 598:
 US-09-721-456-598

Query Match 100.0%; Score 15; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 5 GCTCTAGAAATGAACG 19

RESULT 10
 US-10-325-810-598
 ; Sequence 598, Application US/10325810
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598

Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
|||||
Db 5 GCTCTAGATGAACG 19

RESULT 11

US-10-359-935-23
Sequence 23, Application US/10359935
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
Feng, Junli
Funk, Walter
Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23
Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACG 15
|||||
Db 5 GCTCTAGATGAACG 19
RESULT 12
US-10-330-872-5
Sequence 5, Application US/10330872
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Weinrich, Scott
APPLICANT: Atkinson III, Edward
APPLICANT: Lichtsteiner, Serge
APPLICANT: Vasserot, Alain
APPLICANT: Pruzan, Ronald
TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: 011/006C